

88469

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Nishida

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Dong Jiang (78243)
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U.S. Patent and Trademark Office
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dong.jiang@uspto.gov
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WWW/Internet: _____
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 10.8103 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	92	2	US-08-273-146-45 Sequence 45, Appl
2	42	77.8	92	2	US-08-273-146-53 Sequence 53, Appl
3	42	77.8	107	2	US-08-888-366-14 Sequence 14, Appl
4	42	77.8	107	2	US-08-888-366-20 Sequence 20, Appl
5	42	77.8	107	2	US-08-888-366-26 Sequence 26, Appl
6	42	77.8	109	2	US-08-713-939A-74 Sequence 74, Appl
7	42	77.8	109	4	US-09-036-579-74 Sequence 74, Appl
8	42	77.8	109	4	US-09-550-374-74 Sequence 26, Appl
9	39	72.2	107	3	US-08-483-749A-26 Sequence 6, Appl
10	39	72.2	243	1	US-08-133-804-6 Sequence 6, Appl
11	39	72.2	243	1	US-08-461-838-6 Sequence 6, Appl
12	39	72.2	243	2	US-08-461-386-6 Sequence 6, Appl
13	39	72.2	243	2	US-08-356-786-4 Sequence 4, Appl
14	39	72.2	534	2	US-08-356-786-10 Sequence 10, Appl
15	38	70.4	95	2	US-08-713-939A-72 Sequence 72, Appl
16	38	70.4	95	4	US-09-036-579-72 Sequence 72, Appl
17	38	70.4	95	4	US-09-550-374-72 Sequence 72, Appl
18	38	70.4	109	2	US-08-713-939A-73 Sequence 73, Appl
19	38	70.4	109	4	US-09-036-579-73 Sequence 73, Appl
20	38	70.4	109	4	US-09-550-374-73 Sequence 73, Appl
21	38	70.4	145	4	US-09-096-244-2 Sequence 2, Appl
22	35	64.8	11	1	US-07-942-245-497 Sequence 497, App
23	35	64.8	31	4	US-08-525-539A-3 Sequence 3, Appl
24	35	64.8	107	1	US-08-436-463-20 Sequence 20, Appl
25	35	64.8	107	1	US-08-107-669D-1 Sequence 1, Appl
26	35	64.8	107	1	US-08-472-788A-1 Sequence 1, Appl
27	35	64.8	107	2	US-08-477-531B-1 Sequence 1, Appl

28	35	64.8	107	2	US-08-082-842A-1 Sequence 1, Appli
29	35	64.8	109	1	US-07-942-245-4 Sequence 4, Appli
30	34	63.0	11	1	US-08-137-117D-117 Sequence 117, App
31	34	63.0	11	2	US-08-436-717-117 Sequence 117, App
32	34	63.0	51	1	US-08-472-788A-73 Sequence 73, Appl
33	34	63.0	51	1	US-08-472-788A-74 Sequence 74, Appl
34	34	63.0	51	2	US-08-082-842A-73 Sequence 73, Appl
35	34	63.0	51	2	US-08-082-842A-74 Sequence 74, Appl
36	34	63.0	107	1	US-07-634-278-50 Sequence 50, Appl
37	34	63.0	107	1	US-07-634-278-51 Sequence 51, Appl
38	34	63.0	107	1	US-08-477-728-50 Sequence 50, Appl
39	34	63.0	107	1	US-08-477-728-51 Sequence 51, Appl
40	34	63.0	107	1	US-08-425-336-125 Sequence 125, App
41	34	63.0	107	1	US-08-474-040-50 Sequence 50, Appl
42	34	63.0	107	1	US-08-474-040-51 Sequence 51, Appl
43	34	63.0	107	1	US-08-487-200-50 Sequence 50, Appl
44	34	63.0	107	1	US-08-487-200-51 Sequence 51, Appl
45	34	63.0	107	1	US-08-488-113B-125 Sequence 125, App

ALIGNMENTS

RESULT 1
US-08-273-146-45
; Sequence 45, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-45

Query Match 77.8%; Score 42; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
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 Db 16 RASQDIGSSL 25

RESULT 2

US-08-273-146-53
 ; Sequence 53, Application US/08273146
 ; Patent No. 5855885
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Rodger
 ; APPLICANT: McCafferty, John
 ; APPLICANT: Chiswell, David
 ; APPLICANT: Darsley, Michael J.
 ; APPLICANT: Fitzgerald, Kevin
 ; APPLICANT: Kenten, John H.
 ; APPLICANT: Martin, Mark T.
 ; APPLICANT: Titmas, Richard C.
 ; APPLICANT: Williams, Richard O.
 ; TITLE OF INVENTION: The Isolation and Production of
 ; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IGEN, Inc.
 ; STREET: 1530 East Jefferson St.
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20852
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/273,146
 ; FILING DATE: 14-JUL-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ryan, John W.
 ; REGISTRATION NUMBER: 33,771
 ; REFERENCE/DOCKET NUMBER: 09000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-984-8000
 ; TELEFAX: 301-230-0158
 ; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 92 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-273-146-53

Query Match 77.8%; Score 42; DB 2; Length 92;
 Best Local Similarity 90.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
 |||||
 Db 16 RASQDIGSSL 25

RESULT 3

US-08-888-366-14
 ; Sequence 14, Application US/08888366
 ; Patent No. 5972656
 ; GENERAL INFORMATION:
 ; APPLICANT: Lopez, Osvaldo
 ; APPLICANT: Wylie, Dwane E.
 ; APPLICANT: Wagner, Fred W.
 ; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore

; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/888,366
 ; FILING DATE: 03-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/187,407
 ; FILING DATE: 27-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/990,542
 ; FILING DATE: 14-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/493,299
 ; FILING DATE: 14-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/324,392
 ; FILING DATE: 14-MAR-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Carter, Charles G.
 ; REGISTRATION NUMBER: 35,093
 ; REFERENCE/DOCKET NUMBER: 8648.39USC1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-332-5300
 ; TELEFAX: 612-332-9081
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-888-366-14

Query Match 77.8%; Score 42; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.27;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
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 Db 24 RASQDIGSSL 33

RESULT 4

US-08-888-366-20
 ; Sequence 20, Application US/08888366
 ; Patent No. 5972656
 ; GENERAL INFORMATION:
 ; APPLICANT: Lopez, Osvaldo
 ; APPLICANT: Wylie, Dwane E.
 ; APPLICANT: Wagner, Fred W.
 ; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo

; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-20

Query Match 77.8%; Score 42; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 5

US-08-888-366-26
; Sequence 26, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542

; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-26

Query Match 77.8%; Score 42; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 6

US-08-713-939A-74
; Sequence 74, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match 77.8%; Score 42; DB 2; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 7

US-09-036-579-74
; Sequence 74, Application US/09036579
; Patent No. 6290954

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,579
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,939
; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:

; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-036-579-74

Query Match 77.8%; Score 42; DB 4; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 8

US-09-550-374-74
; Sequence 74, Application US/09550374
; Patent No. 6372214
; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/550,374
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/036,579
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:

; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-550-374-74

Query Match 77.8%; Score 42; DB 4; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 9

US-08-483-749A-26
; Sequence 26, Application US/08483749A
; Patent No. 6054561

; GENERAL INFORMATION:

; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A

;
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-26

Query Match 72.2%; Score 39; DB 3; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 24 RASQDIGNSL 33

RESULT 10
US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-133-804-6

Query Match 72.2%; Score 39; DB 1; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 157 RASQDIGNSL 166
RESULT 11
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-838-6

Query Match 72.2%; Score 39; DB 1; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 157 RASQDIGNSL 166

RESULT 12
US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston

; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-386-6

Query Match 72.2%; Score 39; DB 2; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 157 RASQDIGNSL 166

RESULT 13
US-08-356-786-4
; Sequence 4, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

Query Match 72.2%; Score 39; DB 2; Length 534;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 448 RASQDIGNSL 457

; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-356-786-4

Query Match 72.2%; Score 39; DB 2; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 157 RASQDIGNSL 166

RESULT 14
US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-356-786-10

Query Match 72.2%; Score 39; DB 2; Length 534;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 448 RASQDIGNSL 457

RESULT 15
US-08-713-939A-72
; Sequence 72, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-713-939A-72

Query Match 70.4%; Score 38; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
|||||
Db 10 RASQDFGSSL 19

Search completed: March 10, 2003, 17:02:30
Job time : 10.8103 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 6.87931 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues.

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	92	2	US-08-273-146-45
2	31	100.0	92	2	US-08-273-146-53
3	31	100.0	107	3	US-08-483-749A-26
4	31	100.0	109	1	US-08-466-886-27
5	31	100.0	109	2	US-08-713-939A-74
6	31	100.0	109	4	US-08-469-617-27
7	31	100.0	109	4	US-09-036-579-74
8	31	100.0	109	4	US-09-550-374-74
9	31	100.0	243	1	US-08-133-804-6
10	31	100.0	243	1	US-08-461-838-6
11	31	100.0	243	2	US-08-461-386-6
12	31	100.0	243	2	US-08-356-786-4
13	31	100.0	534	2	US-08-356-786-10
14	31	100.0	694	2	US-08-895-522-3
15	31	100.0	694	3	US-09-195-391-3
16	31	100.0	747	2	US-08-895-522-1
17	31	100.0	747	3	US-09-195-391-1
18	28	90.3	109	1	US-08-466-886-26
19	28	90.3	109	4	US-08-469-617-26
20	28	90.3	1307	1	US-08-395-246C-2
21	28	90.3	1334	2	US-08-996-545-2
22	28	90.3	1334	4	US-09-328-320-2
23	28	90.3	1349	2	US-08-612-734B-2
24	28	90.3	1408	1	US-08-612-521-2
25	27	87.1	105	4	US-08-881-189B-13
26	27	87.1	107	2	US-08-888-366-14
27	27	87.1	107	2	US-08-888-366-20

28	27	87.1	107	2	US-08-888-366-26	Sequence 26, Appl
29	27	87.1	591	4	US-09-199-290-7	Sequence 7, Appli
30	27	87.1	618	4	US-09-199-290-34	Sequence 34, Appl
31	26	83.9	400	4	US-08-961-083-190	Sequence 190, App
32	25	80.6	15	2	US-08-466-860-44	Sequence 44, Appl
33	25	80.6	15	3	US-08-472-040A-44	Sequence 44, Appl
34	25	80.6	15	4	US-08-276-776-44	Sequence 44, Appl
35	25	80.6	15	4	US-08-471-209-44	Sequence 44, Appl
36	25	80.6	107	4	US-09-240-274-29	Sequence 29, Appl
37	25	80.6	109	1	US-08-466-886-24	Sequence 24, Appl
38	25	80.6	109	4	US-08-469-617-24	Sequence 24, Appl
39	25	80.6	110	1	US-08-466-886-20	Sequence 20, Appl
40	25	80.6	110	1	US-08-466-886-21	Sequence 21, Appl
41	25	80.6	110	1	US-08-466-886-22	Sequence 22, Appl
42	25	80.6	110	1	US-08-466-886-23	Sequence 23, Appl
43	25	80.6	110	1	US-08-466-886-25	Sequence 25, Appl
44	25	80.6	110	4	US-08-469-617-20	Sequence 20, Appl
45	25	80.6	110	4	US-08-469-617-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-273-146-45
; Sequence 45, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-45

Query Match 100.0%; Score 31; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||
Db 42 ATSSLDS 48

RESULT 2

US-08-273-146-53
; Sequence 53, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-53

Query Match 100.0%; Score 31; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||
Db 42 ATSSLDS 48

RESULT 3

US-08-483-749A-26
; Sequence 26, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-26

Query Match 100.0%; Score 31; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||
Db 50 ATSSLDS 56

RESULT 4

US-08-466-886-27
; Sequence 27, Application US/08466886
; Patent No. 5776677
; GENERAL INFORMATION:
; APPLICANT: Tsui, Lap-Chee
; APPLICANT: Riordan, John R.
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Kerem, Bat-Sheva
; APPLICANT: Collins, Francis S.
; APPLICANT: Iannuzzi, Michael C.
; APPLICANT: Drumm, Mitchell L.
; APPLICANT: Buckwald, Manuel
; TITLE OF INVENTION: Cystic Fibrosis Gene
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,886
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.

REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.0010006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-466-886-27

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 99 ATSSLDS 105

RESULT 5
US-08-713-939A-74
Sequence 74, Application US/08713939A
Patent No. 5846533
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56
RESULT 6
US-08-469-617-27
Sequence 27, Application US/08469617
Patent No. 6201107
GENERAL INFORMATION:
APPLICANT: Tsui, Lap-Chee
APPLICANT: Riordan, John R.
APPLICANT: Rommens, Johanna M.
APPLICANT: Kerem, Bat-Sheva
APPLICANT: Collins, Francis S.
APPLICANT: Iannuzzi, Michael C.
APPLICANT: Drumm, Mitchell L.
APPLICANT: Buckwald, Manuel
TITLE OF INVENTION: Cystic Fibrosis Gene
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,617
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.0010008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-469-617-27

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 99 ATSSLDS 105

RESULT 7
US-09-036-579-74
Sequence 74, Application US/09036579
Patent No. 6290954
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-579-74

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. NO. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 8
US-09-550-374-74
Sequence 74, Application US/09550374
Patent No. 6372214
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,374
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-74

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. NO. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 9
US-08-133-804-6
Sequence 6, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-133-804-6

Query Match 100.0%; Score 31; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. NO. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

Db 183 ATSSLDS 189
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RESULT 10
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-838-6
Query Match 100.0%; Score 31; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSLDS 7
Db 183 ATSSLDS 189
|||||
RESULT 11
US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts

; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-386-6
Query Match 100.0%; Score 31; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSLDS 7
Db 183 ATSSLDS 189
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RESULT 12
US-08-356-786-4
; Sequence 4, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-4

Query Match 100.0%; Score 31; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 183 ATSSLDS 189

RESULT 13

US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,786

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/831,967

; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Pitcher, Edmund R.

; REGISTRATION NUMBER: 27,829

; REFERENCE/DOCKET NUMBER: CRP-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 534 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-356-786-10

Query Match 100.0%; Score 31; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 474 ATSSLDS 480

RESULT 14

US-08-895-522-3
; Sequence 3, Application US/08895522
; Patent No. 5858719
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE
; TITLE OF INVENTION: TRANSPORT PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/895,522

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0336 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 694 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1167982

US-08-895-522-3

Query Match 100.0%; Score 31; DB 2; Length 694;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 577 ATSSLDS 583

RESULT 15

US-09-195-391-3

; Sequence 3, Application US/09195391

; Patent No. 6080842

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE

; TITLE OF INVENTION: TRANSPORT PROTEIN

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/195,391
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/895,522
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0336 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 694 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 1167982
US-09-195-391-3

Query Match 100.0%; Score 31; DB 3; Length 694;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
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Db 577 ATSSLDS 583

Search completed: March 10, 2003, 17:02:31
Job time : 7.87931 secs

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 8.84483 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	92	2 US-08-273-146-45	Sequence 45, Appl
2	47	100.0	92	2 US-08-273-146-53	Sequence 53, Appl
3	47	100.0	145	4 US-09-096-244-2	Sequence 2, Appl1
4	42	89.4	109	2 US-08-713-939A-74	Sequence 74, Appl
5	42	89.4	109	4 US-09-036-579-74	Sequence 74, Appl
6	42	89.4	109	4 US-09-550-374-74	Sequence 74, Appl
7	40	85.1	95	2 US-08-713-939A-72	Sequence 72, Appl
8	40	85.1	95	4 US-09-036-579-72	Sequence 72, Appl
9	40	85.1	95	4 US-09-550-374-72	Sequence 72, Appl
10	40	85.1	109	2 US-08-713-939A-73	Sequence 73, Appl
11	40	85.1	109	4 US-09-036-579-73	Sequence 73, Appl
12	40	85.1	109	4 US-09-550-374-73	Sequence 73, Appl
13	39	83.0	9	2 US-08-350-260A-503	Sequence 503, App
14	37	78.7	107	1 US-08-276-852-87	Sequence 87, Appl
15	37	78.7	107	1 US-08-899-575-87	Sequence 87, Appl
16	37	78.7	107	1 US-08-899-575-87	Sequence 87, Appl
17	37	78.7	107	5 PCT-US95-08743-87	Sequence 87, Appl
18	36	76.6	108	1 US-08-276-852-99	Sequence 99, Appl
19	36	76.6	108	1 US-08-899-575-99	Sequence 99, Appl
20	36	76.6	108	1 US-08-899-575-99	Sequence 99, Appl
21	36	76.6	108	5 PCT-US95-08743-99	Sequence 99, Appl
22	36	76.6	109	4 US-09-025-769B-16	Sequence 16, Appl
23	35	74.5	53	1 US-08-162-102C-44	Sequence 44, Appl
24	35	74.5	107	3 US-08-483-749A-26	Sequence 26, Appl
25	35	74.5	109	1 US-08-162-102C-24	Sequence 24, Appl
26	35	74.5	109	5 PCT-US93-08786-24	Sequence 24, Appl
27	35	74.5	243	1 US-08-133-804-6	Sequence 6, Appli

28	35	74.5	243	1 US-08-461-838-6	Sequence 6, Appli
29	35	74.5	243	2 US-08-461-386-6	Sequence 6, Appli
30	35	74.5	243	2 US-08-356-786-4	Sequence 4, Appli
31	35	74.5	534	2 US-08-356-786-10	Sequence 10, Appl
32	34	72.3	108	4 US-09-240-274-178	Sequence 178, App
33	33	70.2	9	3 US-08-599-226-14	Sequence 14, Appl
34	33	70.2	9	4 US-09-125-098-14	Sequence 14, Appl
35	32	68.1	9	3 US-08-599-226-19	Sequence 19, Appl
36	32	68.1	9	4 US-09-125-098-19	Sequence 19, Appl
37	32	68.1	23	2 US-08-303-569B-9	Sequence 9, Appli
38	32	68.1	105	3 US-09-065-059-17	Sequence 17, Appl
39	32	68.1	107	2 US-08-561-521-6	Sequence 6, Appli
40	32	68.1	107	2 US-08-561-521-8	Sequence 8, Appli
41	32	68.1	107	2 US-08-652-558-34	Sequence 34, Appl
42	32	68.1	107	2 US-08-652-558-47	Sequence 47, Appl
43	32	68.1	107	2 US-08-318-157B-6	Sequence 6, Appli
44	32	68.1	107	2 US-08-888-366-14	Sequence 14, Appl
45	32	68.1	107	2 US-08-888-366-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-273-146-45
; Sequence 45, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production Of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-45
Query Match 100.0%; Score 47; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.026;


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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 81 LOYASSPYT 89
RESULT 2
US-08-273-146-53
; Sequence 53, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The isolation and production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-53
Query Match 100.0%; Score 47; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOYASSPYT 9
Db 81 LOYASSPYT 89
RESULT 3
US-09-096-244-2
; Sequence 2, Application US/09096244
; Patent No. 6274143
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
; TITLE OF INVENTION: HMEG-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10
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; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,244
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-096-244-2
Query Match 100.0%; Score 47; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOYASSPYT 9
Db 109 LOYASSPYT 117
RESULT 4
US-08-713-939A-74
; Sequence 74, Application US/08713939A
; Patent No 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
```


;
;
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:

;
; INFORMATION FOR SEQ ID NO: 74:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match 89.4%; Score 42; DB 2; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 89 LQYASSPWT 97

RESULT 5

US-09-036-579-74
; Sequence 74, Application US/09036579
; Patent No. 6290954
; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/036,579
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,939

; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807

; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-5277

; TELEFAX: 415-854-0875

; TELEX:

;
; INFORMATION FOR SEQ ID NO: 74:

;
; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids
; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-036-579-74

Query Match 89.4%; Score 42; DB 4; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 89 LQYASSPWT 97

RESULT 6

US-09-550-374-74

; Sequence 74, Application US/09550374
; Patent No. 6372214

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/550,374

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/036,579

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl

; REGISTRATION NUMBER: 28,807

; REFERENCE/DOCKET NUMBER: 06510/059001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-5277

; TELEFAX: 415-854-0875

; TELEX:

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-550-374-74

Query Match 89.4%; Score 42; DB 4; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 89 LQYASSPWT 97

RESULT 7

US-08-713-939A-72

; Sequence 72, Application US/08713939A
; Patent No. 5846533

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road
 CITY: Menlo Park
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/713,939A
 FILING DATE: 13-SEP-1996
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bozicevic, Karl
 REGISTRATION NUMBER: 28,807
 REFERENCE/DOCKET NUMBER: 06510/059001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-5277
 TELEFAX: 415-854-0875
 TELEX:
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 95 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-713-939A-72

Query Match 85.1%; Score 40; DB 2; Length 95;
 Best Local Similarity 77.8%; Pred. No. 0.64;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
 Db 75 LQYAASPF 83

RESULT 8
 US-09-036-579-72
 ; Sequence 72, Application US/09036579
 ; Patent No. 6290954
 ; GENERAL INFORMATION:
 ; APPLICANT: Prusiner, Stanley B.
 ; APPLICANT: Williamson, R. Anthony
 ; APPLICANT: Burton, Dennis R.
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 2200 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/036,579
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/713,939
 ; FILING DATE: 13-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl
 REGISTRATION NUMBER: 28,807
 REFERENCE/DOCKET NUMBER: 06510/059001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-5277
 TELEFAX: 415-854-0875
 TELEX:
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 95 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-036-579-72

Query Match 85.1%; Score 40; DB 4; Length 95;
 Best Local Similarity 77.8%; Pred. No. 0.64;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
 Db 75 LQYAASPF 83

RESULT 9
 US-09-550-374-72
 ; Sequence 72, Application US/09550374
 ; Patent No. 6372214
 ; GENERAL INFORMATION:
 ; APPLICANT: Prusiner, Stanley B.
 ; APPLICANT: Williamson, R. Anthony
 ; APPLICANT: Burton, Dennis R.
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 2200 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/550,374
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/036,579
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bozicevic, Karl
 ; REGISTRATION NUMBER: 28,807
 ; REFERENCE/DOCKET NUMBER: 06510/059001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-854-5277
 ; TELEFAX: 415-854-0875
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 72:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 95 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-550-374-72

Query Match 85.1%; Score 40; DB 4; Length 95;
 Best Local Similarity 77.8%; Pred. No. 0.64;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
||||:|:|

Db 75 LQYAASPFT 83

RESULT 10

US-08-713-939A-73

; Sequence 73, Application US/08713939A

; Patent No. 5846533

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.

; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/713,939A

; FILING DATE: 13-SEP-1996

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl

; REGISTRATION NUMBER: 28,807

; REFERENCE/DOCKET NUMBER: 06510/059001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-5277

; TELEFAX: 415-854-0875

; TELEX:

; INFORMATION FOR SEQ ID NO: 73:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-713-939A-73

Query Match 85.1%; Score 40; DB 2; Length 109;

Best Local Similarity 77.8%; Pred. No. 0.74;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
||||:|:|

Db 89 LQYAASPFT 97

RESULT 11

US-09-036-579-73

; Sequence 73, Application US/09036579

; Patent No. 6290954

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.

; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/036,579

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/713,939

; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl

; REGISTRATION NUMBER: 28,807

; REFERENCE/DOCKET NUMBER: 06510/059001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-5277

; TELEFAX: 415-854-0875

; TELEX:

; INFORMATION FOR SEQ ID NO: 73:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-036-579-73

Query Match 85.1%; Score 40; DB 4; Length 109;

Best Local Similarity 77.8%; Pred. No. 0.74;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
||||:|:|

Db 89 LQYAASPFT 97

RESULT 12

US-09-550-374-73

; Sequence 73, Application US/09550374

; Patent No. 6372214

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.

; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/550,374

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/036,579

; FILING DATE:

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-550-374-73

Query Match      85.1%; Score 40; DB 4; Length 109;
Best Local Similarity 77.8%; Pred. NO. 0.74;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 89 LQYAASPFT 97

RESULT 13
US-08-350-260A-503
; Sequence 503, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 503:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-503

Query Match      83.0%; Score 39; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. NO. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 2 QYGSSPYT 9

RESULT 14
US-08-276-852-87
; Sequence 87, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-87

Query Match 78.7%; Score 37; DB 1; Length 107;
Best Local Similarity 87.5%; Pred. NO. 2.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|| |||||
Db 89 QYHSSPYT 96

RESULT 15
US-08-899-575-87
; Sequence 87, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-87

Query Match 78.7%; Score 37; DB 1; Length 107;
Best Local Similarity 87.5%; Pred. NO. 2.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|| |||||

Db 89 QYHSSPYT 96

Search completed: March 10, 2003, 17:02:31
Job time : 8.84483 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 8.91379 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	54	100.0	11	10	US-09-924-099-3	Sequence 3, Appli
2	54	100.0	108	10	US-09-924-099-1	Sequence 1, Appli
3	54	100.0	237	10	US-09-924-099-9	Sequence 9, Appli
4	54	100.0	243	10	US-09-924-099-10	Sequence 10, Appli
5	42	77.8	109	10	US-09-943-906-74	Sequence 74, Appli
6	42	77.8	130	1	US-08-779-784-35	Sequence 35, Appli
7	39	72.2	243	9	US-09-887-853-6	Sequence 6, Appli
8	39	72.2	267	10	US-09-766-543-10	Sequence 10, Appli
9	39	72.2	276	10	US-09-766-543-12	Sequence 12, Appli
10	38	70.4	11	10	US-09-861-294-6	Sequence 6, Appli
11	38	70.4	88	10	US-09-905-243-30	Sequence 30, Appli
12	38	70.4	95	9	US-10-194-975-91	Sequence 91, Appli
13	38	70.4	95	9	US-10-194-975-92	Sequence 92, Appli
14	38	70.4	95	10	US-09-943-906-72	Sequence 72, Appli
15	38	70.4	109	10	US-09-943-906-73	Sequence 73, Appli
16	38	70.4	145	10	US-09-861-294-2	Sequence 2, Appli
17	36	66.7	11	9	US-09-968-561A-298	Sequence 298, App
18	36	66.7	11	10	US-09-192-854-170	Sequence 170, App
19	35	64.8	31	9	US-09-956-206A-3	Sequence 3, Appli

20	35	64.8	88	10	US-09-905-243-64	Sequence 64, Appli
21	34	63.0	118	10	US-09-811-737-4	Sequence 4, Appli
22	34	63.0	118	10	US-09-811-737-11	Sequence 11, Appli
23	34	63.0	244	10	US-09-940-391-1	Sequence 1, Appli
24	34	63.0	253	10	US-09-811-737-18	Sequence 18, Appli
25	34	63.0	255	10	US-09-811-737-15	Sequence 15, Appli
26	34	63.0	260	10	US-09-811-737-16	Sequence 16, Appli
27	34	63.0	260	10	US-09-811-737-17	Sequence 17, Appli
28	34	63.0	262	10	US-09-811-737-19	Sequence 19, Appli
29	34	63.0	324	10	US-09-815-242-14082	Sequence 14082, A
30	34	63.0	876	9	US-09-712-363-243	Sequence 243, App
31	33	61.1	11	10	US-09-798-058-8	Sequence 8, Appli
32	33	61.1	107	9	US-09-991-470-25	Sequence 25, Appli
33	33	61.1	109	10	US-09-798-058-4	Sequence 4, Appli
34	33	61.1	245	9	US-09-991-470-27	Sequence 27, Appli
35	33	61.1	312	9	US-09-789-054A-22	Sequence 22, Appli
36	33	61.1	315	10	US-09-764-853-772	Sequence 772, App
37	33	61.1	315	10	US-09-764-898-261	Sequence 261, App
38	33	61.1	348	9	US-09-789-054A-20	Sequence 20, Appli
39	33	61.1	348	10	US-09-764-898-188	Sequence 188, App
40	33	61.1	428	10	US-09-886-055-347	Sequence 347, App
41	32	59.3	11	10	US-09-253-794-20	Sequence 20, Appli
42	32	59.3	106	8	US-08-844-215-11	Sequence 11, Appli
43	32	59.3	106	10	US-09-253-794-4	Sequence 4, Appli
44	32	59.3	106	10	US-09-253-794-19	Sequence 19, Appli
45	32	59.3	107	10	US-09-756-301A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-924-099-3
; Sequence 3, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-3

Query Match 100.0%; Score 54; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. NO. 9.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
| | | | | | | | | |
Db 1 RASQDIGSKLY 11

RESULT 2
US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori


```
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match 100.0%; Score 54; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
Db 24 RASQDIGSKLY 34

RESULT 3
US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match 100.0%; Score 54; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
Db 154 RASQDIGSKLY 164

RESULT 4
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
```

```
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match 100.0%; Score 54; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
Db 154 RASQDIGSKLY 164

RESULT 5
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE Prp
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
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;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match      77.8%; Score 42; DB 10; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGSKL 10
      |||||||
Db      24 RASQDIGSSL 33

RESULT 6
US-08-779-784-35
; Sequence 35, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiro
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-35

Query Match      77.8%; Score 42; DB 1; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 RASQDIGSKL 10
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Db      46 RASQDIGSSL 55

RESULT 7
US-09-887-853-6
; Sequence 6, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Blosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match      72.2%; Score 39; DB 9; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGSKL 10
      |||||||
Db      157 RASQDIGNSL 166

RESULT 8
US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543

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; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 267
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Query Match	72.2%;	Score 39;	DB 10;	Length 267;
Best Local Similarity	80.0%;	Pred. NO. 2.8;		
Matches 8; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

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RESULT 9
US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent NO. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TRE
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/7
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,25
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of
; OTHER INFORMATION: linker
US-09-766-543-12

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Query Match      72.2%; Score 39; DB 10; Length 276;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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RESULT 10
US-09-861-294-6
; Sequence 6, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMEG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244

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; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-6

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Query Match	70.4 %;	Score 38;	DB 10;	Length 11;
Best Local Similarity	72.7 %;	Pred. NO. 0.14;		
Matches 8;	Conservative	1;	Mismatches 2;	Indels 0;
				Gaps 0;

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RESULT 11
US-09-905-243-30
; Sequence 30, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-905-243-30

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Query Match 70.4%; Score 38; DB 10; Length 88;
Best Local Similarity 72.7%; Pred. NO. 1.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12
US-10-194-975-91
; Sequence 91, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-194-975-91

Query Match 70.4%; Score 38; DB 9; Length 95;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 RASQDIGSKLY 11
||||| ||| |:
Db 24 RASQSIGSSLH 34

RESULT 13

US-10-194-975-92

; Sequence 92, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-92

Query Match 70.4%; Score 38; DB 9; Length 95;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 RASQDIGSKLY 11
||||| ||| |:
Db 24 RASQSIGSSLH 34

RESULT 14

US-09-943-906-72

; Sequence 72, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-943-906-72

Query Match 70.4%; Score 38; DB 10; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 RASQDIGSKL 10
||||| ||| |:
Db 10 RASQDFGSSL 19

RESULT 15

US-09-943-906-73

; Sequence 73, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-943-906-73

Query Match 70.4%; Score 38; DB 10; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 1 RASQDICKSL 10
 ||||| |
Db 24 RASQDEGSSL 33

Search completed: March 10, 2003, 17:11:27
Job time : 8.91379 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 5.67241 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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14:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	10 US-09-924-099-4	Sequence 4, Appli
2	31	100.0	108	10 US-09-924-099-1	Sequence 1, Appli
3	31	100.0	109	10 US-09-943-906-74	Sequence 74, Appl
4	31	100.0	130	1 US-08-779-784-35	Sequence 35, Appl
5	31	100.0	237	10 US-09-924-099-9	Sequence 9, Appli
6	31	100.0	243	9 US-09-887-853-6	Sequence 6, Appli
7	31	100.0	243	10 US-09-924-099-10	Sequence 10, Appl
8	31	100.0	267	10 US-09-766-543-10	Sequence 10, Appl
9	31	100.0	276	10 US-09-766-543-12	Sequence 12, Appl
10	28	90.3	131	10 US-09-873-409-3	Sequence 3, Appli
11	28	90.3	327	10 US-09-815-242-11463	Sequence 11463, A
12	28	90.3	327	10 US-09-815-242-11625	Sequence 11625, A
13	28	90.3	514	10 US-09-873-409-8	Sequence 8, Appli
14	28	90.3	541	10 US-09-873-409-7	Sequence 7, Appli
15	28	90.3	812	10 US-09-873-409-2	Sequence 2, Appli
16	28	90.3	1058	10 US-09-873-409-4	Sequence 4, Appli
17	28	90.3	1195	10 US-09-873-409-6	Sequence 6, Appli
18	28	90.3	1222	10 US-09-873-409-5	Sequence 5, Appli
19	28	90.3	1334	9 US-09-758-828-2	Sequence 2, Appli

20	28	90.3	1394	9 US-10-101-388-3	Sequence 3, Appli
21	27	87.1	234	9 US-09-764-868-753	Sequence 753, App
22	27	87.1	271	10 US-09-901-884-4	Sequence 4, Appli
23	27	87.1	591	9 US-09-821-616-7	Sequence 7, Appli
24	27	87.1	618	9 US-09-821-616-34	Sequence 34, Appl
25	27	87.1	760	10 US-09-833-017-26	Sequence 26, Appl
26	27	87.1	848	10 US-09-839-185-8	Sequence 8, Appli
27	26	83.9	202	10 US-09-960-253-184	Sequence 184, App
28	26	83.9	400	10 US-09-765-272-190	Sequence 190, App
29	25	80.6	20	10 US-09-982-172-139	Sequence 139, App
30	25	80.6	25	10 US-09-982-172-67	Sequence 67, Appl
31	25	80.6	25	10 US-09-982-172-220	Sequence 220, App
32	25	80.6	107	9 US-09-848-798-29	Sequence 29, Appl
33	25	80.6	167	10 US-09-739-254-125	Sequence 125, App
34	25	80.6	167	10 US-09-904-615-125	Sequence 125, App
35	25	80.6	207	10 US-09-780-717-26	Sequence 26, Appl
36	25	80.6	223	12 US-10-062-254-204	Sequence 204, App
37	25	80.6	339	9 US-09-764-884-25	Sequence 25, Appl
38	25	80.6	351	9 US-10-021-811-10	Sequence 10, Appl
39	25	80.6	353	9 US-09-764-884-33	Sequence 33, Appl
40	25	80.6	458	10 US-09-737-149-28	Sequence 28, Appl
41	25	80.6	475	9 US-10-076-157-4	Sequence 4, Appli
42	25	80.6	501	10 US-09-815-242-13347	Sequence 13347, A
43	25	80.6	543	9 US-09-736-457-337	Sequence 337, App
44	25	80.6	543	9 US-09-902-941-337	Sequence 337, App
45	25	80.6	543	9 US-09-849-626-337	Sequence 337, App

ALIGNMENTS

RESULT 1
US-09-924-099-4
; Sequence 4, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924, 099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-4

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
| | | | | | |
Db 1 ATSSLDS 7

RESULT 2
US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori

; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match 100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 3
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-943-906-74

Query Match 100.0%; Score 31; DB 10; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 4
US-08-779-784-35
; Sequence 35, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-35

Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1' ATSSLDS 7
Db 72 ATSSLDS 78


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; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520C9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match          100.0%; Score 31; DB 10; Length 267;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 202 ATSSLDS 208

RESULT 9
US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9sFv plus
; OTHER INFORMATION: linker
US-09-766-543-12

Query Match          100.0%; Score 31; DB 10; Length 276;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 202 ATSSLDS 208

RESULT 10
US-09-873-409-3
; Sequence 3, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
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; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-3

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Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 106 ATSSALDS 112

RESULT 11
US-09-815-242-11463
; Sequence 11463, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11463
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11463

Query Match          90.3%; Score 28; DB 10; Length 327;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 165 ATSSALDS 171

RESULT 12
US-09-815-242-11625
; Sequence 11625, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
```


; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11625
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11625

Query Match 90.3%; Score 28; DB 10; Length 327;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||:||||
Db 165 ATSALDS 171

RESULT 13

US-09-873-409-8
; Sequence 8, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-8

Query Match 90.3%; Score 28; DB 10; Length 514;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
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Db 489 ATSALDS 495

RESULT 14

US-09-873-409-7
; Sequence 7, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:

; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: NO. US20020037522A1e
; LOCATION: (230)..(230)
; OTHER INFORMATION: Xaa at position 230 represents any L amino acid
US-09-873-409-7

Query Match 90.3%; Score 28; DB 10; Length 541;
Best Local Similarity 85.7%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||:||||
Db 516 ATSALDS 522

RESULT 15

US-09-873-409-2
; Sequence 2, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-2

Query Match 90.3%; Score 28; DB 10; Length 812;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||:||||
Db 106 ATSALDS 112

Search completed: March 10, 2003, 17:11:28
Job time : 6.67241 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 7.2931 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues 188354
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published_Applications_AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	47	100.0	9	10	US-09-861-294-10
2	47	100.0	9	10	US-09-924-099-5
3	47	100.0	108	10	US-09-924-099-1
4	47	100.0	130	1	US-08-779-784-35
5	47	100.0	145	10	US-09-861-294-2
6	47	100.0	237	10	US-09-924-099-9
7	47	100.0	243	10	US-09-924-099-10
8	42	89.4	109	10	US-09-943-906-74
9	40	85.1	95	10	US-09-943-906-72
10	40	85.1	109	10	US-09-943-906-73
11	35	74.5	243	9	US-09-887-853-6
12	35	74.5	267	10	US-09-766-543-10
13	35	74.5	276	10	US-09-766-543-12
14	35	74.5	559	9	US-09-866-050A-499
15	34	72.3	107	8	US-08-844-215-12
16	34	72.3	108	9	US-09-848-798-178
17	34	72.3	405	10	US-09-864-761-38102
18	33	70.2	121	9	US-09-797-941A-4
19	33	70.2	245	9	US-09-797-941A-6

20	33	70.2	303	9	US-09-510-332-125	Sequence 125, Appli
21	32	68.1	23	9	US-09-795-515-9	Sequence 9, Appli
22	32	68.1	107	9	US-09-999-025-15	Sequence 15, Appli
23	32	68.1	107	9	US-09-999-040-15	Sequence 15, Appli
24	32	68.1	107	9	US-09-998-817-15	Sequence 15, Appli
25	32	68.1	107	9	US-09-999-021-15	Sequence 15, Appli
26	32	68.1	107	9	US-10-040-997-15	Sequence 15, Appli
27	32	68.1	107	10	US-09-253-794-6	Sequence 6, Appli
28	32	68.1	108	10	US-09-229-200A-14	Sequence 14, Appli
29	32	68.1	569	10	US-09-765-272-154	Sequence 154, App
30	32	68.1	591	10	US-09-765-272-74	Sequence 74, Appli
31	31	66.0	88	9	US-09-862-540-41	Sequence 41, Appli
32	31	66.0	107	9	US-09-874-141-1	Sequence 1, Appli
33	31	66.0	107	9	US-09-874-141-2	Sequence 2, Appli
34	31	66.0	107	9	US-09-874-141-3	Sequence 3, Appli
35	31	66.0	107	9	US-09-874-141-4	Sequence 4, Appli
36	31	66.0	107	9	US-09-874-141-9	Sequence 9, Appli
37	31	66.0	111	10	US-09-920-171-7	Sequence 7, Appli
38	31	66.0	133	9	US-09-874-141-45	Sequence 45, Appli
39	31	66.0	133	9	US-09-874-141-47	Sequence 47, Appli
40	31	66.0	133	9	US-09-874-141-51	Sequence 51, Appli
41	31	66.0	150	9	US-09-782-397-5	Sequence 5, Appli
42	31	66.0	287	9	US-09-782-397-17	Sequence 17, Appli
43	31	66.0	304	9	US-09-782-397-14	Sequence 14, Appli
44	31	66.0	352	10	US-09-912-020-293	Sequence 293, App
45	31	66.0	2310	10	US-09-995-542-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-861-294-10
; Sequence 10, Application US/09861294
; Patent No.: US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFg AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-10

Query Match 100.0%; Score 47; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
| | | | | | | |
Db 1 LQYASSPYT 9

RESULT 2
US-09-924-099-5
; Sequence 5, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi

;
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-09-861-294-2

Query Match 100.0%; Score 47; DB 10; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | |
Db 109 LOYASSPYT 117

RESULT 6

US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match 100.0%; Score 47; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | |
Db 219 LOYASSPYT 227

RESULT 7

US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33

; SEQ ID NO. 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match 100.0%; Score 47; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | |
Db 219 LOYASSPYT 227

RESULT 8

US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-943-906-74

Query Match 89.4%; Score 42; DB 10; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | |
Db 89 LOYASSPWT 97

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RESULT 9
US-09-943-906-72
; Sequence 72, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;      Williamson, R. Anthony
;      Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-943-906-72

Query Match      85.1%; Score 40; DB 10; Length 95;
Best Local Similarity 77.8%; Pred. No. 0.76;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQYASSPYT 9
      ||||:|:|
Db      75 LQYAASPFT 83

RESULT 10
US-09-943-906-73
; Sequence 73, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;      Williamson, R. Anthony
;      Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
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; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-943-906-73

Query Match      85.1%; Score 40; DB 10; Length 109;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQYASSPYT 9
      ||||:|:|
Db      89 LQYAASPFT 97

RESULT 11
US-09-887-853-6
; Sequence 6, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
;      Oppermann, Hermann
;      Houston, L. L.
;      Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
;      NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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;
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100

;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 74.5%; Score 35; DB 9; Length 243;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||||
Db 222 LQYAIFPYT 230

RESULT 12
US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520C9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match 74.5%; Score 35; DB 10; Length 267;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||||
Db 241 LQYAIFPYT 249

RESULT 13
US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20

;
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9sFv plus
; OTHER INFORMATION: linker
US-09-766-543-12

Query Match 74.5%; Score 35; DB 10; Length 276;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||||
Db 241 LQYAIFPYT 249

RESULT 14
US-09-866-050A-499
; Sequence 499, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 499
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Rat
US-09-866-050A-499

Query Match 74.5%; Score 35; DB 9; Length 559;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||||
Db 325 LQNASAPYT 333

RESULT 15
US-08-844-215-12
; Sequence 12, Application US/08844215
; Patent No. US20020016445A1
; GENERAL INFORMATION:
; APPLICANT: PERSSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/844,215
;; FILING DATE: 17-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/635,109
;; FILING DATE: 19-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MCCracken, THOMAS P.
;; REGISTRATION NUMBER: 38,548
;; REFERENCE/DOCKET NUMBER: 80146.002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 325-7812
;; TELEFAX: (650) 325-7823
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-844-215-12

Query Match 72.3%; Score 34; DB 8; Length 107;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 90 QYGSPPYT 97

Search completed: March 10, 2003, 17:11:28
Job time : 7.2931 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 31.1034 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	AA44589	Mouse anti-IL-18 a
2	54	100.0	108	AA44587	Mouse anti-IL-18 a
3	54	100.0	135	AA44599	Mouse light chain
4	54	100.0	237	AA44595	EscFv#125-2H recom
5	54	100.0	243	AA44596	EscFv#125-2H.HT re
6	42	77.8	90	AA80078	Mouse derived ligh
7	42	77.8	92	AAW95480	Mouse derived RT3
8	42	77.8	92	AAW95476	Mouse derived RT3
9	42	77.8	107	AAW78972	Light chain variab
10	42	77.8	107	AAW79247	Light chain variab

11	42	77.8	107	16	AAW79250	Light chain variab
12	42	77.8	107	18	AAW27121	Murine antibody li
13	42	77.8	108	13	AAW21310	Light chain of Mlf
14	42	77.8	109	18	AAW18271	Prp 37 light chain
15	42	77.8	109	20	AAW85910	Prp 37 light chain
16	42	77.8	109	22	AAG65862	Anti-Prp antibody
17	42	77.8	109	23	ABP51796	Anti-prion protein
18	42	77.8	252	23	AAU72863	P4-14 single chain
19	42	77.8	257	23	AAU72869	P5-11 single chain
20	42	77.8	499	23	AAU72872	3B10xP4-14 bispeci
21	41	75.9	109	20	AAW06388	Humanised LM609 an
22	41	75.9	109	20	AAW06382	Humanised LM609 an
23	39	72.2	107	21	AAW90824	520C9 hybridoma VL
24	39	72.2	112	23	AAW50879	Anti-bovine prion
25	39	72.2	243	17	AAW02280	520C9 anti-c-erbB-
26	39	72.2	243	19	AAW53170	520C9 anti-c-erbB-
27	39	72.2	246	14	AAW80424	520C9 sfv sequence
28	39	72.2	267	22	AAU04944	Sequence of 520C9
29	39	72.2	267	22	AAU04944	Humanised anti-pl8
30	39	72.2	409	22	AAU04945	Humanised anti-pl8
31	39	72.2	534	14	AAW39571	Sequence of G-FIT.
32	38	70.4	11	23	ABB77068	AC2885 antibody li
33	38	70.4	88	21	AAW56653	Partial peptide fr
34	38	70.4	95	18	AAW18269	Prp 81 light chain
35	38	70.4	95	20	AAW85908	Prp 81 light chain
36	38	70.4	95	22	AAG65860	Anti-Prp antibody
37	38	70.4	95	23	ABP51794	Anti-prion protein
38	38	70.4	109	18	AAW18270	Prp 28 light chain
39	38	70.4	109	20	AAW85909	Prp 28 light chain
40	38	70.4	109	22	AAG65861	Anti-Prp antibody
41	38	70.4	109	23	ABP51795	Anti-prion protein
42	38	70.4	126	23	ABB77064	AC2885 antibody li
43	38	70.4	128	21	AAW56718	Amino acid sequenc
44	38	70.4	145	18	AAW27119	Murine monoclonal
45	38	70.4	145	20	AAW87593	Antibody 11D10 lig

ALIGNMENTS

RESULT 1

AA44589

ID AA44589 standard; Protein; 11 AA.

XX

AC AA44589;

XX

DT 04-APR-2000 (first entry)

XX

DE Mouse anti-IL-18 antibody VL complementarity-determining region-1.

XX

KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
complementarity-determining region; CDR; hybridoma #125-2H; mouse;
monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;
KW immunosuppressive; leucocytopoietic; antialgic; antipyretic;
KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
KW inflammatory disorder; immunoreaction.

XX

OS Mus musculus.

XX

PN EP974600-A2.

XX

PD 26-JAN-2000.

XX

PF 24-JUN-1999; 99EP-0304977.

XX

PR 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.

PR 22-DEC-1998; 98JP-0365023.

XX

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX

PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49536.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 7; Page 18; 36pp; English.
XX
CC The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-Interleukin-18 antibody light chain variable region
CC (VL) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2HmAb, which is capable of neutralising biological activities of
CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
CC leucocytopenetic, antialgic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
Db 1 RASQDIGSKLY 11

RESULT 2
AA44587
ID AAY44587 standard; Protein; 108 AA.
XX
AC AAY44587;
XX
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse anti-IL-18 antibody light chain variable region.
XX
KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
KW antiinflammatory; immunosuppressive; leucocytopenetic; antialgic;
KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
KW immunopathy; inflammatory disorder; immunoreaction.
XX
OS Mus musculus.
XX
XX EP974600-A2.
PN
XX 26-JAN-2000.
PD
XX 24-JUN-1999; 99EP-0304977.
PF
XX 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
PI
XX WPI; 2000-118341/11.
DR N-PSDB; AAZ49534.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 5; Page 17; 36pp; English.
XX
CC The present protein sequence is the mouse anti-Interleukin-18 antibody

CC light chain variable region (VL) encoded by cDNA derived from hybridoma
CC #125-2H. The nucleotide sequence is used in the production of recombinant
CC monoclonal antibody #125-2HmAb, which is capable of neutralising
CC biological activities of interleukin-18. The antibody has antialgic,
CC antiinflammatory, immunosuppressive, leucocytopenetic, antipyretic,
CC antiallergic and hepatotropic activity and can be used for prevention and
CC treatment of autoimmune diseases, immunopathies and inflammatory
CC disorders caused by excessive immunoreaction.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
Db 24 RASQDIGSKLY 34

RESULT 3
AAY44599
ID AAY44599 standard; Protein; 135 AA.
XX
AC AAY44599;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse light chain variable region encoded by PCR A product.
XX
KW Mouse light chain variable region; VL; variable region light chain;
KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
KW hematopoietic; leucocytopenetic; antialgic; antipyretic.
XX
OS Mus musculus.
OS Synthetic.
XX
XX EP974600-A2.
PN
XX 26-JAN-2000.
PD
XX 24-JUN-1999; 99EP-0304977.
PF
XX 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
PI
XX WPI; 2000-118341/11.
DR N-PSDB; AAZ49548.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Disclosure; Page 28-29; 32pp; English.
XX
CC The present sequence is the mouse light chain variable region. This was
CC encoded by a recombinant DNA is derived from PCR A which amplifies
CC antibody light chain variable region (VL). The transformant produced
CC using the VL gene was used to transform competent E. coli cells. The peptide
CC produced by transformants neutralises interleukin-18. This is useful for
CC treating and preventing immunopathies, inflammatory disorders and
CC autoimmune diseases which are caused by excessive immunoreaction. The
CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
CC hematopoietic, leucocytopenetic, antialgic, antipyretic and hepatic
CC -function improving activities.
XX
SQ Sequence 135 AA;

Query Match 100.0%; Score 54; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
|||||
Db 44 RASQDIGSKLY 54

RESULT 4
AAY44595
ID AAY44595 standard; Protein; 237 AA.
XX
AC AAY44595;
XX

DT 04-APR-2000 (first entry)
XX

DE EscFv#125-2H recombinant protein.
XX

KW EscFv#125-2H recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.
XX

OS Mus musculus.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"
XX

PN EP974600-A2.
XX

PD 26-JAN-2000.
XX

XX
PF 24-JUN-1999; 99EP-0304977.
XX

PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49542.
XX
XX

PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX

PS Claim 8; Page 19-20; 32pp; English.
XX

CC The present sequence is EscFv#125-2H protein encoded by recombinant cDNA
CC pEscFv#125-2H for neutralising interleukin-18. The protein is produced
CC from hybridoma #125-2H by transforming pEscFv#125-2H in competent
CC E. coli cells. This is useful for treating and preventing immunopathies,
CC inflammatory disorders and autoimmune diseases which are caused by
CC excessive immunoreaction. The protein has anti-allergic,
CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,
CC antialgic, antipyretic and hepatic-function improving activities.
XX

SQ Sequence 237 AA;

Query Match 100.0%; Score 54; DB 21; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
|||||
Db 154 RASQDIGSKLY 164

RESULT 5
AAY44596

ID AAY44596 standard; Protein; 243 AA.
XX
AC AAY44596;
XX

DT 04-APR-2000 (first entry)
XX

DE EscFv#125-2H.HT recombinant protein.
XX

KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.
XX

OS Mus musculus.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"
XX

PN EP974600-A2.
XX

PD 26-JAN-2000.
XX

XX
PF 24-JUN-1999; 99EP-0304977.
XX

PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49543.
XX
XX

PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX

PS Claim 8; Page 20-21; 32pp; English.
XX

CC The present sequence is EscFv#125-2H.HT protein encoded by
CC recombinant cDNA pEscFv#125-2H.HT for neutralising interleukin-18. The
CC protein is produced from hybridoma #125-2H by transforming
CC pEscFv#125-2H.HT in competent E. coli cells. There are six histidine
CC residues positioned after the light chain variable region. This protein
CC is useful for treating and preventing immunopathies, inflammatory
CC disorders and autoimmune diseases which are caused by excessive
CC immunoreaction. The protein has anti-allergic, anti-inflammatory,
CC immunosuppressive, hematopoietic, leukocytopoietic, antialgic,
CC antipyretic and hepatic-function improving activities.
XX

SQ Sequence 243 AA;

Query Match 100.0%; Score 54; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11

Db 154 RASQDIGSKLY 164

|||||

RESULT 6

AAR80078

ID AAR80078 standard; Protein; 90 AA.

XX

AC AAR80078;

XX

DT 22-MAY-1996 (first entry)

XX

DE Mouse derived light chain RT3 phage antibody pattern A.

XX

KW Light chain; RT3; murine; catalytic antibody; bacteriophage;

KW pattern A.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Region 1..15

FT /note= "framework region 1"

FT Region 16..26

FT /note= "complementarity determining region 1"

FT Region 27..40

FT /note= "framework region 2"

FT Region 41..47

FT /note= "complementarity determining region 2"

FT Region 48..78

FT /note= "framework region 3"

FT Region 79..88

FT /note= "complementarity determining region 3"

FT Region 89..90

FT /note= "framework region 4

FT N-terminal fragment"

XX

PN W09527045-A1.

XX

PD 12-OCT-1995.

XX

PF 30-MAR-1994; 94WO-US03420.

XX

PR 30-MAR-1994; 94WO-US03420.

XX

PA (IGEN-) IGEN INC.

XX

PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;

XX

DR WPI; 1995-358624/46.

DR N-PSDB; AAT04625.

XX

PT Production of catalytic antibodies displayed on phage - by

PT generating a gene library of antibody-derived domains and expressing

PT it in phage vectors

XX

PS Disclosure; Fig 9; 133pp; English.

XX

CC AAT04625 encodes AAR80078 mouse derived light chain RT3 phage antibody.

CC The DNA was used in the prepn. of catalytic antibody (CA) producing

CC bacteriophage. The CAs can be used to activate/deactivate a

CC biological function in an animal by enhancing the rate of cleavage,

CC or formation of a specific bond within a mol. in vivo.

XX

SQ Sequence 90 AA;

Query Match 77.8%; Score 42; DB 16; Length 90;

Best Local Similarity 90.0%; Pred. No. 0.87;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10

|||||

Db 16 RASQDIGSSL 25

RESULT 7

AAW95480

ID AAW95480 standard; Protein; 92 AA.

XX

AC AAW95480;

XX

DT 29-MAR-1999 (first entry)

XX

DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.

XX

KW Catalytic; antibody; phage display; immunising; phage expression vector;

KW prodrug; scFV.

XX

OS Mus sp.

XX

PN US5855885-A.

XX

PD 05-JAN-1999.

XX

PF 14-JUL-1994; 94US-0273146.

XX

PR 22-JAN-1993; 93US-0007684.

PR 14-JUL-1994; 94US-0273146.

XX

PA (CHIS/) CHISWELL D.

PA (DARS/) DARSLEY M J.

PA (FITZ/) FITZGERALD K.

PA (KENT/) KENTEN J H.

PA (MART/) MARTIN M T.

PA (MCCA/) MCCAFFERTY J.

PA (SMIT/) SMITH R.

PA (TITM/) TITMAS R C.

PA (WILL/) WILLIAMS R O.

XX

PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;

XX

DR WPI; 1999-105036/09.

DR N-PSDB; AAX00879.

XX

PT Production of catalytic antibodies displayed on bacteriophages -

PT comprises generating a gene library of antibody-derived domains

PT inserting coding into a phage expression vector and isolating the

PT catalytic antibodies

XX

PS Example 4; Fig 11; 117pp; English.

XX

CC The invention relates to methods for producing catalytic antibodies

CC displayed on a phage. The method comprises: (a) generating a gene library

CC of antibody-derived domains; (b) inserting coding for the domains into a

CC phage expression vector; and (c) isolating the catalytic antibodies. The

CC phage expression vector incorporates a histidine peptide in tandem with a

CC myc peptide. The catalytic antibodies can be isolated by preparing an

CC antigen; optionally immunising an animal with the antigen; generating a

CC library of VH and VL domains from the immunised animal; cloning the VH

CC and VL domains into a phage expression vector to generate phage display

CC antibodies; selecting phage display antibodies which bind specifically

CC to the antigen; screening the selected phage display antibodies for

CC catalytic activity to substrate; and isolating the catalytic antibodies,

CC where the phage expression vector incorporates a histidine peptide in

CC tandem with a myc peptide. The processes are used to produce catalytic

CC antibodies, which can be used for in vivo activation of a prodrug. The

CC present sequence represents a genetic sequence of light chain PCR

CC pattern C from mouse derived RT3 phage antibodies.

XX

SQ Sequence 92 AA;

Query Match 77.8%; Score 42; DB 20; Length 92;

Best Local Similarity 90.0%; Pred. No. 0.89;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 16 RASQDIGSSL 25

RESULT 8
AAW95476
ID AAW95476 standard; Protein; 92 AA.
XX
AC AAW95476;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern A genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW prodrug; scFv.
XX
OS Mus sp.
XX
PN US5855885-A.
XX
PD 05-JAN-1999.
XX
PF 14-JUL-1994; 94US-0273146.
XX
PR 22-JAN-1993; 93US-0007684.
PR 14-JUL-1994; 94US-0273146.
XX
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX
DR WPI; 1999-105036/09.
DR N-PSDB; AAX00875.
XX
PT Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains
PT inserting coding into a phage expression vector and isolating the
PT catalytic antibodies
XX
PS Example 4; Fig 9A-F; 117pp; English.
XX
CC The invention relates to methods for producing catalytic antibodies
CC displayed on a phage. The method comprises: (a) generating a gene library
CC of antibody-derived domains; (b) inserting coding for the domains into a
CC phage expression vector; and (c) isolating the catalytic antibodies. The
CC phage expression vector incorporates a histidine peptide in tandem with a
CC myc peptide. The catalytic antibodies can be isolated by preparing an
CC antigen; optionally immunising an animal with the antigen; generating a
CC library of VH and VL domains from the immunised animal; cloning the VH
CC and VL domains into a phage expression vector to generate phage display
CC antibodies; selecting phage display antibodies which bind specifically
CC to the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a prodrug. The
CC present sequence represents a genetic sequence of light chain pattern A
CC from mouse derived RT3 phage antibodies.
XX
SQ Sequence 92 AA;

Query Match 77.8%; Score 42; DB 20; Length 92;

Best Local Similarity 90.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 16 RASQDIGSSL 25

RESULT 9
AAR78972
ID AAR78972 standard; Protein; 107 AA.
XX
AC AAR78972;
XX
DT 21-DEC-1995 (first entry)
XX
DE Light chain variable region for monoclonal antibody 5B6.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW light chain.
XX
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
DR WPI; 1995-275415/36.
DR N-PSDB; AAQ97510.
XX
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX
PS Claim 23; Page 70; 106pp; English.
XX
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MABs that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
XX
SQ Sequence 107 AA;

Query Match 77.8%; Score 42; DB 16; Length 107;
Best Local Similarity 90.0%; Pred. No. 1;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 10
AAR79247
ID AAR79247 standard; Protein; 107 AA.
XX
AC AAR79247;
XX
DT 21-DEC-1995 (first entry)
XX
DE Light chain variable region for monoclonal antibody 1F10.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW light chain.
XX
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
XX WPI; 1995-275415/36.
DR N-PSDB; AAQ97504.
XX

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX

PS Claim 23; Page 62; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MABs that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
XX

SQ Sequence 107 AA;

Query Match 77.8%; Score 42; DB 16; Length 107;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 11
AAR79250
ID AAR79250 standard; Protein; 107 AA.
XX
AC AAR79250;
XX
DT 21-DEC-1995 (first entry)
XX
DE Light chain variable region for monoclonal antibody 5G4.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW light chain.
XX
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
XX WPI; 1995-275415/36.
DR N-PSDB; AAQ97507.
XX

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX

PS Claim 23; Page 66; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MABs that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
XX

SQ Sequence 107 AA;

Query Match 77.8%; Score 42; DB 16; Length 107;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
 | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 12
AAW27121
ID AAW27121 standard; Protein; 107 AA.
XX
AC AAW27121;
XX
DT 04-JAN-1998 (first entry)
XX
DE Murine antibody light chain variable region consensus.
XX
KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMEG; tumour; breast cancer; vaccine.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..56
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 88..96
FT /label= CDR3
FT /note= "complementarity determining region 3"
XX
PN WO9722699-A2.
XX
PD 26-JUN-1997.
XX
PF 19-DEC-1996; 96WO-US20757.
XX
PR 13-DEC-1996; 96US-0575762.
PR 20-DEC-1995; 95US-0575762.
PR 26-JAN-1996; 96US-0591965.
XX
PA (KENT) UNIV KENTUCKY.
XX
PI Chatterjee M, Chatterjee SK, Foon KA;
XX
DR WPI; 1997-341690/31.
XX
PT Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
PT against human milk fat globule disease associated tumours,
PT especially breast cancer
XX
PS Example 2; Fig 26C; 130pp; English.
XX
CC This polypeptide sequence comprises a consensus sequence of murine
CC light chain variable regions (VL) selected on the basis of identity
CC to the VL region (see W27119) of monoclonal anti-idiotypic antibody
CC 11D10. The sequences were obtained from a GenBank database
CC search. A VH consensus (W27122) was also produced. 11D10 has at
CC least 18 departures from the consensus sequences (7 in the light
CC chain and 11 in the heavy chain). 8 Occur within CDRs and 10
CC outside CDRs. 11D10 polypeptides and polynucleotides can be
CC used in vaccines and pharmaceutical compositions for the treatment
CC of human milk fat globule-associated diseases such as breast
CC cancer.
XX
SQ Sequence 107 AA;

Query Match 77.8%; Score 42; DB 18; Length 107;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
 | | | | | | | |

Db 24 RASQDIGSSL 33

RESULT 13
AAR21310
ID AAR21310 standard; Protein; 108 AA.
XX
AC AAR21310;
XX
DT 21-MAY-1992 (first entry)
XX
DE Light chain of Mlf clone.
XX
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 25..34
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 89..96
FT /label= CDR3
XX
PN WO9201047-A.
XX
PD 23-JAN-1992.
XX
PF 10-JUL-1991; 91WO-GB01134.
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonner TP;
XX
DR WPI; 1992-056862/07.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 46; Fig 52; 109pp; English.
XX
CC The sequence is the light chain of clone M1F encoding an scFv frag-
CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC The DNA encoding the chain was amplified from a cDNA library prepd.
CC from the spleen of an unimmunised mouse. The corresponding heavy
CC chain was also amplified from an existing construct, pSWL-VHD1.3
CC (Ward et al, 1989). The two fragments were assembled via a linker
CC to prepare an scFv construct which was ligated into the fdCAT2
CC vector for expression on the surface of fd bacteriophage. In this
CC way, the VL domain was replaced by a library of VL domains to allow
CC for selection of a broader range of antibody specificities. Several
CC clones were isolated which bound to TEL (the parent antibody D1.3
CC binds exclusively to HEL). The sequences of the light chains of
CC two of these clones, MFI and M21 are given in AAR21310 and AAR21311
CC respectively. The D1.3 light chain is given in AAR21309.
CC See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.
XX
SQ Sequence 108 AA;

Query Match 77.8%; Score 42; DB 13; Length 108;

Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 14
AAW18271
ID AAW18271 standard; peptide; 109 AA.
XX
AC AAW18271;
XX
DT 09-JAN-1998 (first entry)
XX
DE PrP 37 light chain variable region.
XX
KW Prion protein; Prp; heavy chain variable region; antibody; scrapie;
KW light chain variable region; Prp-Sc; pathogen; fatal familial insomnia;
KW central nervous system spongiform encephalopathy; human; therapy;
KW transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
KW bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW Serstmann-Strassler-Scheinker Disease.
XX
OS Mus musculus.
XX

FH Key Location/Qualifiers
FT Region 1..23
FT /note= "framework region 1"
FT Region 24..34
FT /note= "complementarity determining region 1"
FT Region 35..49
FT /note= "framework region 2"
FT Region 50..56
FT /note= "complementarity determining region 2"
FT Region 57..88
FT /note= "framework region 3"
FT Region 89..97
FT /note= "complementarity determining region 3"
FT Region 98..109
FT /note= "framework region 4"

XX WO9710505-A1.
PN
XX
XX
PD 20-MAR-1997.
XX
PF 13-SEP-1996; 96WO-US14840.
XX
XX 14-SEP-1995; 95US-0528104.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Burton DR, Prusiner SB, Williamson RA;
PI
XX WPI; 1997-202357/18.
DR
XX
XX New antibodies to the scrapie isoform of prion protein - used for
PT detection of infectious prion proteins or for treating disease such
PT as BSE, CJD or scrapie
XX
XX Example 9; Fig 6; 99pp; English.
PS
XX

AAW18266-W18285 represent portions of the antibodies of the invention.
CC The antibodies of the invention are able to bind the scrapie isoform of
CC prion protein Prp-Sc in situ. Prions are infectious pathogens that cause
CC central nervous system spongiform encephalopathies in humans and
CC animals. The scrapie isoform of the prion protein (Prp-Sc) is necessary
CC for both the transmission and pathogenesis of the transmissible
CC neurodegenerative diseases of animals and humans. The antibodies can be
CC used in a method of the invention for detecting human Prp-Sc in a source.
CC The antibodies specifically bind to prion proteins associated with
CC disease and do not bind to denatured PrP proteins not associated with

CC disease. They can bind to prion proteins of a specific species of
CC mammals. They can also have the ability to neutralise infectious prions.
CC The antibodies can be used for screening for the presence of prions in
CC products such as pharmaceuticals, food or cosmetics. They can also be
CC used for prion neutralisation to purify products, for extraction of prion
CC proteins or for therapy, for diseases such as bovine spongiform
CC encephalopathy, Creutzfeldt-Jakob Disease, fatal familial insomnia or
CC Serstmann-Strassler-Scheinker Disease, scrapie or feline spongiform
CC encephalopathies.
XX
SQ Sequence 109 AA;
XX

Query Match 77.8%; Score 42; DB 18; Length 109;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 15
AAW85910
ID AAW85910 standard; peptide; 109 AA.
XX
AC AAW85910;
XX

DT 12-FEB-1999 (first entry)
XX
DE PrP 37 light chain variable region.
XX
KW PrP; PrP(Sc); scrapie; isoform; antibody; prion; CJD; screening;
KW Creutzfeldt-Jakob disease; infectivity; assay; pharmaceutical; food;
KW cosmetic; therapeutic; mouse.
XX

OS Mus sp.
XX

FH Key Location/Qualifiers
FT Region 1..23
FT /note= "Framework 1"
FT Region 24..34
FT /note= "complementarity determining region 1 (CDR1)"
FT Region 35..49
FT /note= "Framework 2"
FT Region 50..56
FT /note= "complementarity determining region 2 (CDR2)"
FT Region 57..88
FT /note= "Framework 3"
FT Region 89..97
FT /note= "complementarity determining region 3 (CDR3)"
FT Region 98..109
FT /note= "Framework 4"

XX US5846533-A.
PN
XX
XX PD 08-DEC-1998.
DR
XX
XX 13-SEP-1996; 96US-0713939.
PF
XX
XX 13-SEP-1996; 96US-0713939.
PR
XX 14-SEP-1995; 95US-0528104.
DR
XX (SCRI) SCRIPPS RES INST.
PA (REGC) UNIV CALIFORNIA.
XX
XX Burton DR, Prusiner SB, Williamson RA;
PI
XX WPI; 1999-058996/05.
DR
XX Antibody specific for scrapie isoform of prion protein - useful for
PT diagnosis and therapy
XX
PS Example 9; Fig 6A-B; 58pp; English.

XX The invention relates to an antibody that is capable of binding to
CC native PrP(Sc), the scrapie isoform of prion protein (PrP). The antibody
CC is produced by a method that comprises synthesising a library of
CC antibodies on phages, contacting the phages with a composition containing
CC PrP proteins, isolating phages that bind to native PrP(Sc) in situ,
CC obtaining an antibody from the phages, and optionally analysing the
CC phages to determine a nucleic acid sequence encoding an amino acid
CC sequence to which the native PrP(Sc) binds. The antibody is used to
CC detect disease- associated PrP, especially in Creutzfeldt-Jakob disease
CC (CJD) and distinguish it from normal PrP. They can also be used to
CC neutralise the infectivity of PrP(Sc). Assays using the antibodies can be
CC used to screen for disease-associated PrP in pharmaceutical products,
CC cosmetics and foods or for therapeutic purposes. Sequences AAW85908 to
CC AAW85910 represent light chain variable regions of the phage clones
CC generated by panning an IgG1 library from mouse D7282 against denatured
CC PrP.

XX
SQ Sequence 109 AA;

Query Match 77.8%; Score 42; DB 20; Length 109;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

Search completed: March 10, 2003, 16:56:55
Job time : 32.1034 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 19.7931 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	AAW70945	CDR2 of the light
2	31	100.0	7	AAW44590	Mouse anti-IL-18 a
3	31	100.0	90	AAR80078	Mouse derived ligh
4	31	100.0	92	AAW95480	Mouse derived RT3
5	31	100.0	92	AAW95476	Mouse derived RT3
6	31	100.0	95	AAW70954	Light chain of mon
7	31	100.0	97	ABP33764	Human transport pr
8	31	100.0	107	AAW27121	Murine antibody li
9	31	100.0	107	AAW90824	520C9 hybridoma VL
10	31	100.0	108	AAR21310	Light chain of Mlf

11	31	100.0	108	21	AAW44587	Mouse anti-IL-18 a
12	31	100.0	109	18	AAW18271	Prp 37 light chain
13	31	100.0	109	20	AAW85910	Prp 37 light chain
14	31	100.0	109	22	AAG65862	Anti-Prp antibody
15	31	100.0	109	23	ABP51796	Anti-prion protein
16	31	100.0	112	23	AAW50879	Anti-bovine prion
17	31	100.0	135	21	AAW44599	Mouse light chain
18	31	100.0	146	4	AAP30251	Sequence of the le
19	31	100.0	147	22	AAG75566	Human colon cancer
20	31	100.0	237	21	AAW44595	EscFv#125-2H recom
21	31	100.0	243	17	AAW02280	520C9 anti-c-erbB-
22	31	100.0	243	19	AAW53170	520C9 anti-c-erbB-
23	31	100.0	243	20	AAW80424	520C9 sfv sequence
24	31	100.0	243	21	AAW44596	EscFv#125-2H.HT re
25	31	100.0	246	14	AAR39569	Sequence of 520C9
26	31	100.0	252	23	AAU72863	P4-14 single chain
27	31	100.0	257	23	AAU72869	P5-11 single chain
28	31	100.0	267	22	AAU04944	Humanised anti-pl8
29	31	100.0	409	22	AAU04945	Humanised anti-pl8
30	31	100.0	499	23	AAU72872	3B10xP4-14 bispeci
31	31	100.0	555	22	AAG70797	S cerevisiae apopt
32	31	100.0	606	22	ABB57811	Drosophila melanog
33	31	100.0	606	22	ABB57812	Drosophila melanog
34	31	100.0	722	22	AAB92941	Human protein sequ
35	31	100.0	747	20	AAW89585	Human ATP-binding
36	31	100.0	747	21	AAB13355	Human ATP-binding
37	31	100.0	752	20	AAW14068	Human ABC-transport
38	29	93.5	1552	22	ABB71764	Drosophila melanog
39	29	93.5	1561	22	ABG22379	Novel human diagno
40	29	93.5	1792	22	AAW39065	Human polypeptide
41	29	93.5	1870	22	ABG22378	Novel human diagno
42	29	93.5	2447	22	ABG22380	Novel human diagno
43	28	90.3	80	21	AAW52602	Helicobacter pylori
44	28	90.3	272	18	AAW20101	H. pylori transpor
45	28	90.3	285	18	AAW20861	H. pylori cell env

ALIGNMENTS

RESULT 1
AAW70945
ID AAW70945 standard; peptide; 7 AA.
XX AAW70945;
XX 14-OCT-1998 (first entry)
XX CDR2 of the light chain of monoclonal antibody RS-255.
KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX Synthetic.
OS Mus sp.
XX FR2758331-A1.
XX 17-JUL-1998.
XX 14-JAN-1997; 97FR-0000300.
XX 14-JAN-1997; 97FR-0000300.
XX (UYBO-) UNIV BOURGOGNE.
PI Bourgeois C, Kohli E, Pothier P;
XX WPI; 1998-390320/34.
XX New peptide(s) recognising viral epitope with tropism to mucosa -

PT useful for, e.g. diagnosing, preventing and treating viral
PT infection(s)
XX
PS Claim 12; Page 39; 5lpp; French.
XX
CC AAW70905-46 represent peptide sequences that can recognise, by
CC antigen-antibody type reactions, at least 1 epitope of a pathogenic
CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are
CC analogous to CDR regions of monoclonal antibodies specific for
CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR
CC regions of monoclonal antibodies specific for site III or IV of the
CC VP6 protein of rota virus (RV). The peptides can neutralise viral
CC infections and may also inhibit fusion between infected and uninfected
CC cells or cells and viruses. They provide passive or active protection
CC and/or inhibit transcription of the virus, so are useful as antiviral
CC agents or for prophylaxis, in human or veterinary medicine. The peptides
CC can be labelled and used to diagnose infection or contamination by the
CC virus. The peptides are particularly directed against RSV or RS but may
CC also be used against papilloma, adeno, entero, polio, influenza or
CC immune deficiency viruses.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSLDS 7
Db | | | | | | |
1 ATSSLDS 7
RESULT 2
AAAY44590
ID AAY44590 standard; Protein; 7 AA.
XX
AC AAAY44590;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse anti-IL-18 antibody VL complementarity-determining region-2.
XX
KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW complementarity-determining region; CDR; hybridoma #125-2H; mouse;
KW monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;
KW immunosuppressive; leucocytopenic; antialgic; antipyretic;
KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
KW inflammatory disorder; immunoreaction.
XX
OS Mus musculus.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49537.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 7; Page 18; 36pp; English.

XX The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-Interleukin-18 antibody light chain variable region
CC (VL) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2HmAb, which is capable of neutralising biological activities of
CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
CC leucocytopenic, antialgic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSLDS 7
Db | | | | | | |
1 ATSSLDS 7
RESULT 3
AAR80078
ID AAR80078 standard; Protein; 90 AA.
XX
AC AAR80078;
XX
DT 22-MAY-1996 (first entry)
XX
DE Mouse derived light chain RT3 phage antibody pattern A.
XX
KW Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW pattern A.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1..15 /note= "framework region 1"
FT Region 16..26 /note= "complementarity determining region 1"
FT Region 27..40 /note= "framework region 2"
FT Region 41..47 /note= "complementarity determining region 2"
FT Region 48..78 /note= "framework region 3"
FT Region 79..88 /note= "complementarity determining region 3"
FT Region 89..90 /note= "framework region 4
FT /note= N-terminal fragment"
XX
PN WO9527045-A1.
XX
PD 12-OCT-1995.
XX
PF 30-MAR-1994; 94WO-US03420.
XX
PR 30-MAR-1994; 94WO-US03420.
XX
PA (IGEN-) IGEN INC.
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
XX
DR WPI; 1995-358624/46.
DR N-PSDB; AAT04625.
XX
PT Production of catalytic antibodies displayed on phage - by
PT generating a gene library of antibody-derived domains and expressing

PT it in phage vectors
XX
PS Disclosure; Fig 9; 133pp; English.
XX
CC AAT04625 encodes AAR80078 mouse derived light chain RT3 phage antibody.
CC The DNA was used in the prepn. of catalytic antibody (CA) producing
CC bacteriophage. The CAs can be used to activate/deactivate a
CC biological function in an animal by enhancing the rate of cleavage,
CC or formation of a specific bond within a mol. in vivo.
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 31; DB 16; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 41 ATSSLDS 47

RESULT 4
AAW95480
ID AAW95480 standard; Protein; 92 AA.
XX
AC AAW95480;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW prodrug; scFV.
XX
OS Mus sp.
XX
PN US5855885-A.
XX
PD 05-JAN-1999.
XX
PF 14-JUL-1994; 94US-0273146.
XX
PR 22-JAN-1993; 93US-0007684.
PR 14-JUL-1994; 94US-0273146.
XX
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX
DR WPI; 1999-105036/09.
DR N-PSDB; AAX00879.
XX
PT Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains
PT inserting coding into a phage expression vector and isolating the
PT catalytic antibodies
XX
PS Example 4; Fig 11; 117pp; English.
XX
CC The invention relates to methods for producing catalytic antibodies
CC displayed on a phage. The method comprises: (a) generating a gene library
CC of antibody-derived domains; (b) inserting coding for the domains into a
CC phage expression vector; and (c) isolating the catalytic antibodies. The
CC phage expression vector incorporates a histidine peptide in tandem with a

CC myc peptide. The catalytic antibodies can be isolated by preparing an
CC antigen; optionally immunising an animal with the antigen; generating a
CC library of VH and VL domains from the immunised animal; cloning the VH
CC and VL domains into a phage expression vector to generate phage display
CC antibodies; selecting phage display antibodies which bind specifically
CC to the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a prodrug. The
CC present sequence represents a genetic sequence of light chain PCR
CC pattern C from mouse derived RT3 phage antibodies.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 31; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 42 ATSSLDS 48

RESULT 5
AAW95476
ID AAW95476 standard; Protein; 92 AA.
XX
AC AAW95476;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern A genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW prodrug; scFV.
XX
OS Mus sp.
XX
PN US5855885-A.
XX
PD 05-JAN-1999.
XX
PF 14-JUL-1994; 94US-0273146.
XX
PR 22-JAN-1993; 93US-0007684.
PR 14-JUL-1994; 94US-0273146.
XX
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX
DR WPI; 1999-105036/09.
DR N-PSDB; AAX00875.
XX
PT Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains
PT inserting coding into a phage expression vector and isolating the
PT catalytic antibodies
XX
PS Example 4; Fig 9A-F; 117pp; English.
XX
CC The invention relates to methods for producing catalytic antibodies
CC displayed on a phage. The method comprises: (a) generating a gene library

CC of antibody-derived domains; (b) inserting coding for the domains into a
CC phage expression vector; and (c) isolating the catalytic antibodies. The
CC phage expression vector incorporates a histidine peptide in tandem with a
CC myc peptide. The catalytic antibodies can be isolated by preparing an
CC antigen; optionally immunising an animal with the antigen; generating a
CC library of VH and VL domains from the immunised animal; cloning the VH
CC and VL domains into a phage expression vector to generate phage display
CC antibodies; selecting phage display antibodies which bind specifically
CC to the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a prodrug. The
CC present sequence represents a genetic sequence of light chain pattern A
CC from mouse derived RT3 phage antibodies.

XX Sequence 92 AA;

Query Match 100.0%; Score 31; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
| | | | |
Db 42 ATSSLDS 48

RESULT 6
AAW70954
ID AAW70954 standard; protein; 95 AA.
XX
AC AAW70954;

DT 14-OCT-1998 (first entry)

XX Light chain of monoclonal antibody RS-255.

DE Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

XX Mus sp.

OS FR2758331-A1.

XX 17-JUL-1998.

PD 14-JAN-1997; 97FR-0000300.

XX 14-JAN-1997; 97FR-0000300.

PF (UYBO-) UNIV BOURGOGNE.

PR Bourgeois C, Kohli E, Pothier P;

XX WPI; 1998-390320/34.

DR New peptide(s) recognising viral epitope with tropism to mucosa -
PT useful for, e.g. diagnosing, preventing and treating viral
PT infection(s)

XX Disclosure; Fig 2; 51pp; French.

PS The present sequence represents the light chain of monoclonal antibody
CC RS-255, which is directed against the respiratory syncytial virus (RSV).
CC The specification describes peptides which recognise, by
CC antigen-antibody type reactions, at least 1 epitope of a pathogenic virus
CC having tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous
CC to CDR regions of monoclonal antibodies specific for RSV. AAW70917-28 are
CC analogous to CDR regions of monoclonal antibodies specific for site III
CC or IV of the VP6 protein of rota virus (RV). The peptides can neutralise
CC viral infections and may also inhibit fusion between infected and

CC uninfected cells or cells and viruses. They provide passive or active
CC protection and/or inhibit transcription of the virus, so are useful as
CC antiviral agents or for prophylaxis, in human or veterinary medicine. The
CC peptides can be labelled and used to diagnose infection or contamination
CC by the virus. The peptides are particularly directed against RSV or RS
CC but may also be used against papilloma, adeno, entero, polio, influenza
CC or immune deficiency viruses.

XX Sequence 95 AA;

Query Match 100.0%; Score 31; DB 19; Length 95;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
| | | | |
Db 37 ATSSLDS 43

RESULT 7
ABP33764
ID ABP33764 standard; Protein; 97 AA.
XX
AC ABP33764;

XX 08-JUL-2002 (first entry)

DE Human transport protein-like ORF2737 protein, SEQ ID NO:5474.

XX Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide.

XX Homo sapiens.

OS WO200190366-A2.

XX 29-NOV-2001.

PD 24-MAY-2001; 2001WO-US17076.

XX 24-MAY-2000; 2000US-206690P.

PR (CURA-) CURAGEN CORP.

XX Leach MD, Shimkets RA;

PI WPI; 2002-106200/14.

DR N-PSDB; ABN77790.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation

PS Claim 10; Page 1619-1620; 2508pp; English.

XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN79587 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX

CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases.

SQ Sequence 97 AA;

Query Match 100.0%; Score 31; DB 23; Length 97;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||

Db 52 ATSSLDS 58

RESULT 8

AAW27121
ID AAW27121 standard; Protein; 107 AA.

XX

AC AAW27121;

XX

DT 04-JAN-1998 (first entry)

XX

DE Murine antibody light chain variable region consensus.

XX

KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMFg; tumour; breast cancer; vaccine.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1
FT /note= "complementarity determining region 1"

FT Region 50..56

FT /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 88..96

FT /label= CDR3

FT /note= "complementarity determining region 3"

XX

PN WO9722699-A2.

XX

PD 26-JUN-1997.

XX

PF 19-DEC-1996; 96WO-US20757.

XX

PR 13-DEC-1996; 96US-0575762.

PR 20-DEC-1995; 95US-0575762.
PR 26-JAN-1996; 96US-0591965.
XX
PA (KENT) UNIV KENTUCKY.
XX
PI Chatterjee M, Chatterjee SK, Foon KA;
XX WPI; 1997-341690/31.
XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
PT against human milk fat globule disease associated tumours,
PT especially breast cancer
XX
PS Example 2; Fig 26C; 130pp; English.

XX This polypeptide sequence comprises a consensus sequence of murine

CC light chain variable regions (VL) selected on the basis of identity

CC to the VL region (see W27119) of monoclonal anti-idiotypic antibody

CC 11D10. The sequences were obtained from a GenBank database

CC search. A VH consensus (W27122) was also produced. 11D10 has at

CC least 18 departures from the consensus sequences (7 in the light

CC chain and 11 in the heavy chain). 8 Occur within CDRs and 10

CC outside CDRs. 11D10 polypeptides and polynucleotides can be

CC used in vaccines and pharmaceutical compositions for the treatment

CC of human milk fat globule-associated diseases such as breast

CC cancer.

XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 31; DB 18; Length 107;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||

Db 50 ATSSLDS 56

RESULT 9

AAW90824
ID AAW90824 standard; Protein; 107 AA.

XX

AC AAW90824;

XX

DT 29-AUG-2000 (first entry)

XX

DE 520C9 hybridoma VL domain SEQ ID NO:26.

XX

KW Antigen binding site; immunoglobulin; cancer antigen; immunological;
KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
KW specific binding assay; affinity purification; drug targeting;
KW toxin targeting; imaging; genetic; therapeutic.

OS Homo sapiens.

XX

PN US6054561-A.

XX

PD 25-APR-2000.

XX

PF 07-JUN-1995; 95US-0483749.

XX

PR 21-MAR-1986; 86US-0842476.

PR 08-MAY-1988; 88US-0190778.

PR 08-FEB-1984; 84US-0577976.

PR 11-JAN-1985; 85US-0690750.

PR 11-AUG-1994; 94US-0288981.

XX

PA (CHIR) CHIRON CORP.

XX

PI Ring DB;

XX

PR WPI; 2000-338508/29.

DR

N-PSDB; AAA38908.

XX Monoclonal antibody capable of binding to human breast cancer antigen
PT useful for affinity purification, drug or toxin targeting, imaging, and
PT treating cancer -
XX
PS Disclosure; Fig 13; 57pp; English.
XX
CC The present invention describes a monoclonal antibody (MAB) (I) that
CC binds to a human breast cancer antigen that is also bound by Mab 454C11
CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
CC described is a hybridoma that produces (I). (I) is useful in specific
CC binding assays, affinity purification, drug or toxin targeting, imaging,
CC and genetic or immunological therapeutics for various cancers. The
CC present sequence represents a VL domain derived from a 520C9 hybridoma,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 31; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 10
AAR21310
ID AAR21310 standard; Protein; 108 AA.
XX
AC AAR21310;
XX
XX 21-MAY-1992 (first entry)
XX Light chain of Mlf clone.
DE
XX
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 25..34
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 89..96
FT /label= CDR3
XX
PN WO9201047-A.
XX
XX 23-JAN-1992.
PD
XX
XX 10-JUL-1991; 91WO-GB01134.
PF
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnert TP;
XX
XX WPI; 1992-056862/07.
DR
XX
XX Producing members of specific binding pairs - by expression in

PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 46; Fig 52; 109pp; English.
XX
CC The sequence is the light chain of clone M1F encoding an scFv frag-
CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC The DNA encoding the chain was amplified from a cDNA library prepd.
CC from the spleen of an unimmunised mouse. The corresponding heavy
CC chain was also amplified from an existing construct, PSW1-VHD1.3
CC (Ward et al, 1989). The two fragments were assembled via a linker
CC to prepare an scFv construct which was ligated into the fdCAT2
CC vector for expression on the surface of fd bacteriophage. In this
CC way, the VL domain was replaced by a library of VL domains to allow
CC for selection of a broader range of antibody specificities. Several
CC clones were isolated which bound to TEL (the parent antibody D1.3
CC binds exclusively to HEL). The sequences of the light chains of
CC two of these clones, MFI and M21 are given in AAR21310 and AAR21311
CC respectively. The D1.3 light chain is given in AAR21309.
CC See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 31; DB 13; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 11
AAY44587
ID AAY44587 standard; Protein; 108 AA.
XX
AC AAY44587;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse anti-IL-18 antibody light chain variable region.
XX
KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
KW antiinflammatory; immunosuppressive; leucocytopenetic; antialgic;
KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
KW immunopathy; inflammatory disorder; immunoreaction.
XX
OS Mus musculus.
XX
PN EP974600-A2.
XX
XX 26-JAN-2000.
PD
XX
XX 24-JUN-1999; 99EP-0304977.
PF
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
PI
XX WPI; 2000-118341/11.
DR
XX N-PSDB; AAZ49534.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 5; Page 17; 36pp; English.
XX

CC The present protein sequence is the mouse anti-Interleukin-18 antibody
CC light chain variable region (VL) encoded by cDNA derived from hybridoma
CC #125-2H. The nucleotide sequence is used in the production of recombinant
CC monoclonal antibody #125-2HmAb, which is capable of neutralising
CC biological activities of interleukin-18. The antibody has antialgic,
CC antiinflammatory, immunosuppressive, leucocytopoietic, antipyretic,
CC antiallergic and hepatotropic activity and can be used for prevention and
CC treatment of autoimmune diseases, immunopathies and inflammatory
CC disorders caused by excessive immunoreaction.

XX SQ Sequence 108 AA;
Query Match 100.0%; Score 31; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||
Db 50 ATSSLDS 56

RESULT 12
AAW18271
ID AAW18271 standard; peptide; 109 AA.

XX AC AAW18271;

XX DT 09-JAN-1998 (first entry)

XX DE PrP 37 light chain variable region.

XX KW Prion protein; Prp; heavy chain variable region; antibody; scrapie;
KW light chain variable region; Prp-Sc; pathogen; fatal familial insomnia;
KW central nervous system spongiform encephalopathy; human; therapy;
KW transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
KW bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW Serstmann-Strassler-Scheinker Disease.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Region 1..23

FT Region /note= "framework region 1"

FT Region /note= "complementarity determining region 1"

FT Region /note= "framework region 2"

FT Region /note= "complementarity determining region 2"

FT Region /note= "framework region 3"

FT Region /note= "complementarity determining region 3"

FT Region /note= "framework region 4"

XX WO9710505-A1.

XX PD 20-MAR-1997.

XX PF 13-SEP-1996; 96WO-US14840.

XX PR 14-SEP-1995; 95US-0528104.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Burton DR, Prusiner SB, Williamson RA;

XX DR WPI; 1997-202357/18.

XX PT New antibodies to the scrapie isoform of prion protein - used for
PT detection of infectious prion proteins or for treating disease such
PT as BSE, CJD or scrapie

XX PS Example 9; Fig 6; 99pp; English.

XX CC AAW18266-W18285 represent portions of the antibodies of the invention.
CC The antibodies of the invention are able to bind the scrapie isoform of
CC prion protein PrP-Sc in situ. Prions are infectious pathogens that cause
CC central nervous system spongiform encephalopathies in humans and
CC animals. The scrapie isoform of the prion protein (PrP-Sc) is necessary
CC for both the transmission and pathogenesis of the transmissible
CC neurodegenerative diseases of animals and humans. The antibodies can be
CC used in a method of the invention for detecting human PrP-Sc in a source.
CC The antibodies specifically bind to prion proteins associated with
CC disease and do not bind to denatured PrP proteins not associated with
CC disease. They can bind to prion proteins of a specific species of
CC mammals. They can also have the ability to neutralise infectious prions.
CC The antibodies can be used for screening for the presence of prions in
CC products such as pharmaceuticals, food or cosmetics. They can also be
CC used for prion neutralisation to purify products, for extraction of prion
CC proteins or for therapy, for diseases such as bovine spongiform
CC encephalopathy, Creutzfeldt-Jakob Disease, fatal familial insomnia or
CC Serstmann-Strassler-Scheinker Disease, scrapie or feline spongiform
CC encephalopathies.

XX SQ Sequence 109 AA;

Query Match 100.0%; Score 31; DB 18; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||
Db 50 ATSSLDS 56

RESULT 13
AAW85910

ID AAW85910 standard; peptide; 109 AA.

XX AC AAW85910;

XX DT 12-FEB-1999 (first entry)

XX DE PrP 37 light chain variable region.

XX KW PrP; PrP(Sc); scrapie; isoform; antibody; prion; CJD; screening;
KW Creutzfeldt-Jakob disease; infectivity; assay; pharmaceutical; food;
KW cosmetic; therapeutic; mouse.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Region 1..23

FT Region /note= "Framework 1"

FT Region /note= "complementarity determining region 1 (CDR1)"

FT Region /note= "Framework 2"

FT Region /note= "complementarity determining region 2 (CDR2)"

FT Region /note= "Framework 3"

FT Region /note= "complementarity determining region 3 (CDR3)"

FT Region /note= "Framework 4"

XX US5846533-A.

XX PN 08-DEC-1998.

XX PF 13-SEP-1996; 96US-0713939.

XX PR 13-SEP-1996; 96US-0713939.

PR 14-SEP-1995; 95US-0528104.
XX (SCRI) SCRIPPS RES INST.
PA (REGC) UNIV CALIFORNIA.
XX
PI Burton DR, Prusiner SB, Williamson RA;
XX
XX WPI; 1999-058996/05.
DR
XX
XX Antibody specific for scrapie isoform of prion protein - useful for
PT diagnosis and therapy
PT
XX
PS Example 9; Fig 6A-B; 58pp; English.
XX
CC The invention relates to an antibody that is capable of binding to
CC native PrP(Sc), the scrapie isoform of prion protein (PrP). The antibody
CC is produced by a method that comprises synthesising a library of
CC antibodies on phages, contacting the phages with a composition containing
CC PrP proteins, isolating phages that bind to native PrP(Sc) in situ,
CC obtaining an antibody from the phages, and optionally analysing the
CC phages to determine a nucleic acid sequence encoding an amino acid
CC sequence to which the native PrP(Sc) binds. The antibody is used to
CC detect disease- associated PrP, especially in Creutzfeldt-Jakob disease
CC (CJD) and distinguish it from normal PrP. They can also be used to
CC neutralise the infectivity of PrP(Sc). Assays using the antibodies can be
CC used to screen for disease-associated PrP in pharmaceutical products,
CC cosmetics and foods or for therapeutic purposes. Sequences AAW85908 to
CC AAW85910 represent light chain variable regions of the phage clones
CC generated by panning an IgG1 library from mouse D7282 against denatured
CC PrP.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 31; DB 20; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db ||||||
50 ATSSLDS 56

RESULT 14
AAG65862
ID AAG65862 standard; peptide; 109 AA.
XX
AC AAG65862;
XX
DT 11-FEB-2002 (first entry)
XX
DE Anti-PrP antibody light chain variable region fragment.
XX
KW PrP; prion protein; Creutzfeldt-Jakob disease; familial insomnia; PrP-Sc;
KW scrapie; Gerstmann-Strassler-Scheinker disease; anti-PrP antibody.
XX
OS Mus sp.
XX
PN US6290954-B1.
XX
PD 18-SEP-2001.
XX
PF 06-MAR-1998; 98US-0036579.
XX
PR 13-SEP-1996; 96US-0713939.
PR 14-SEP-1995; 95US-0528104.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Prusiner SB, Williamson RA, Burton DR;
XX
XX WPI; 2001-637939/73.
XX
PT Detecting a scrapie isoform of the prion protein (PrP-Sc) in a source,

PT particularly useful for detecting e.g. Creutzfeldt-Jakob disease or
PT Gerstmann-Strassler-Scheinker disease, by contacting the source with
PT PrP-Sc antibodies
XX
PS Example 9; Fig 6A-B; 58pp; English.
XX
CC The invention provides a method for detecting a scrapie isoform of the
CC prion protein (PrP-Sc) in a source. The method involves contacting the
CC source suspected of containing native PrP-Sc with a diagnostic amount of
CC an antibody characterized by its ability to bind to native PrP-Sc in
CC situ. The method is useful for detecting PrP-Sc in a source, which is
CC particularly useful for detecting Creutzfeldt-Jakob disease, fatal
CC familial insomnia or Gerstmann-Strassler-Scheinker disease. Sequences
CC AAG65856-862 represent amino acid sequences of heavy and light chain
CC variable regions of anti-PrP antibodies.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 31; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db ||||||
50 ATSSLDS 56

RESULT 15
ABP51796
ID ABP51796 standard; Protein; 109 AA.
XX
AC ABP51796;
XX
DT 03-OCT-2002 (first entry)
XX
DE Anti-prion protein (PrP) antibody related protein SEQ ID NO:74.
XX
KW Prion protein; PrP; scrapie; PrPSc; prion disease; immunoassay;
KW detection; anti-prion protein antibody; anti-PrP antibody.
XX
OS Mus sp.
OS Synthetic.
XX
PN US6372214-B1.
XX
PD 16-APR-2002.
XX
PF 13-APR-2000; 2000US-0550374.
XX
PR 13-SEP-1996; 96US-0713939.
PR 06-MAR-1998; 98US-0036579.
PR 14-SEP-1995; 95US-0528104.
XX
PA (REGC) UNIV CALIFORNIA.
PA (SCRI) SCRIPPS RES INST.
XX
PI Prusiner SB, Williamson RA, Burton DR;
XX
XX WPI; 2002-433675/46.
DR
XX
PT Immunoassays for detecting scrapie isoforms of prion protein (PrPSc)
PT and for purifying PrPSc from samples, useful e.g. in diagnosing PrPSc
PT disease and testing pharmaceuticals for contamination
XX
PS Example 9; Fig 6; 58pp; English.
XX
CC The present invention describes methods for detecting scrapie isoforms
CC of prion protein (PrPSc) infection in dead animals, purifying materials
CC suspected of containing PrPSc proteins and treating materials, using
CC antibodies specific for PrPSc. Also described: (1) method of determining
CC PrPSc infection in a dead animal, comprising: (a) extracting tissue from
CC an animal that has died; (b) contacting the tissue with an antibody
CC characterised by its ability to bind to native PrPSc in situ (the

CC antibody binds to a form of PrPsc specific to the animal that has died);
CC and (c) determining if the antibody has bound to PrPsc (the presence of
CC PrPsc in the tissue is indicative of PrPsc infection); (2) a method of
CC purifying a material suspected of containing a PrPsc protein, comprising:
CC (a) contacting the material with an antibody (characterized by its
CC ability to bind native PrPsc in situ) which is bound to a support
CC surface; and (b) removing material not bound to the antibody; (3) a
CC method of treating a material, comprising applying (to the material) an
CC antibody that binds native PrPsc in situ. The methods are used for
CC diagnosing and detecting prion disease (scrapie) in dead animal tissue
CC (i.e. immunoassays), for separating PrPsc proteins from biological
CC samples (i.e. immunopurification) and for treating materials. The present
CC sequence represents an anti-prion protein (PrP) antibody related protein
CC sequence, which is used in an example from the present invention.

xx

SQ Sequence 109 AA;

Query Match 100.0%; Score 31; DB 23; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||

Db 50 ATSSLDS 56

Search completed: March 10, 2003, 16:56:56
Job time : 20.7931 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 25.4483 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	21 AAY44591	Mouse anti-IL-18 a
2	47	100.0	90	16 AAR80078	Mouse derived ligh
3	47	100.0	90	16 AAR80079	Mouse derived ligh
4	47	100.0	92	20 AAW95480	Mouse derived RT3
5	47	100.0	92	20 AAW95476	Mouse derived RT3
6	47	100.0	107	18 AAW27121	Murine antibody li
7	47	100.0	108	21 AAY44587	Mouse anti-IL-18 a
8	47	100.0	135	21 AAY44599	Mouse light chain
9	47	100.0	145	18 AAW27119	Murine monoclonal
10	47	100.0	145	20 AAW87593	Antibody l1d10 lig

11	47	100.0	237	21	AAY44595	EscFv#125-2H recom
12	47	100.0	243	21	AAY44596	EscFv#125-2H.HT re
13	47	100.0	252	23	AAU72863	P4-14 single chain
14	47	100.0	257	23	AAU72869	p5-11 single chain
15	47	100.0	499	23	AAU72872	3B10xP4-14 bispeci
16	43	91.5	9	19	AAW70946	CDR3 of the light
17	43	91.5	95	19	AAW70954	Light chain of mon
18	42	89.4	108	13	AAW21310	Light chain of Mlf
19	42	89.4	109	18	AAW18271	Prp 37 light chain
20	42	89.4	109	20	AAW85910	Prp 37 light chain
21	42	89.4	109	22	AAG65862	Anti-Prp antibody
22	42	89.4	109	23	ABP51796	Anti-prion protein
23	42	89.4	146	4	AAP30251	Sequence of the le
24	40	85.1	95	18	AAW18269	Prp 81 light chain
25	40	85.1	95	20	AAW85908	Prp 81 light chain
26	40	85.1	95	22	AAG65860	Anti-Prp antibody
27	40	85.1	95	23	ABP51794	Anti-prion protein
28	40	85.1	109	18	AAW18270	Prp 28 light chain
29	40	85.1	109	20	AAW85909	Prp 28 light chain
30	40	85.1	109	22	AAG65861	Anti-Prp antibody
31	40	85.1	109	23	ABP51795	Anti-prion protein
32	40	85.1	312	22	ABB09185	Acinetobacter calc
33	40	85.1	321	22	ABB09186	Acinetobacter calc
34	39	83.0	107	22	AAB62771	Human HIV-1 monocl
35	39	83.0	129	14	AAR38672	Vk325-Jk2. Homo s
36	37	78.7	107	15	AAR54308	Anti-HIV gp120 imm
37	37	78.7	107	17	AAW01266	VL region of HIV n
38	37	78.7	107	21	AAY95118	Anti-gp120 antibod
39	37	78.7	107	21	AAY98227	Anti-gp120 antibod
40	37	78.7	113	21	AAB18855	Amino acid sequenc
41	37	78.7	113	21	AAB18867	Amino acid sequenc
42	37	78.7	113	21	AAB18875	Amino acid sequenc
43	37	78.7	113	21	AAB18877	Amino acid sequenc
44	36	76.6	9	18	AAW24551	CDR #3 of r101-2 l
45	36	76.6	108	15	AAR54316	Anti-HIV gp120 imm

ALIGNMENTS

RESULT 1

AY44591
ID AY44591 standard; Protein; 9 AA.

XX AY44591;

XX AC AY44591;

XX DT 04-APR-2000 (first entry)

XX DE Mouse anti-IL-18 antibody VL complementarity-determining region-3.

XX KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL; complementarity-determining region; CDR; hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory; immunosuppressive; leucocytopenic; antialgic; antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy; inflammatory disorder; immunoreaction.

XX OS Mus musculus.

XX PN EP974600-A2.

XX PD 26-JAN-2000.

XX PF 24-JUN-1999; 99EP-0304977.

XX PR 24-JUN-1998; 98JP-0177580.

XX PR 12-OCT-1998; 98JP-0289044.

XX PR 22-DEC-1998; 98JP-0365023.

XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX XX

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49538.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 7; Page 18; 36pp; English.
XX
CC The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-interleukin-18 antibody light chain variable region
CC (VL) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2HmAb, which is capable of neutralising biological activities of
CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
CC leucocytopenetic, antialgic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
IIIIIIIIII
Db 1 LQYASSPYT 9

RESULT 2
AAR80078
ID AAR80078 standard; Protein; 90 AA.

XX
AC AAR80078;
XX
DT 22-MAY-1996 (first entry)
XX
DE Mouse derived light chain RT3 phage antibody pattern A.
XX
KW Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW pattern A.
XX
OS Mus musculus.

XX
FH Key Location/Qualifiers
FT Region 1..15
FT /note= "framework region 1"
FT Region 16..26
FT /note= "complementarity determining region 1"
FT Region 27..40
FT /note= "framework region 2"
FT Region 41..47
FT /note= "complementarity determining region 2"
FT Region 48..78
FT /note= "framework region 3"
FT Region 79..88
FT /note= "complementarity determining region 3"
FT Region 89..90
FT /note= "framework region 4
FT N-terminal fragment"

XX WO9527045-A1.
XX
XX 12-OCT-1995.
XX
XX 30-MAR-1994; 94WO-US03420.
XX
XX 30-MAR-1994; 94WO-US03420.
XX
XX (IGEN-) IGEN INC.
PA
XX

PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
XX
DR WPI; 1995-358624/46.
DR N-PSDB; AAT04625.
XX
PT Production of catalytic antibodies displayed on phage - by
PT generating a gene library of antibody-derived domains and expressing
PT it in phage vectors
XX
PS Disclosure; Fig 9; 133pp; English.
XX
CC AAT04625 encodes AAR80078 mouse derived light chain RT3 phage antibody.
CC The DNA was used in the prepn. of catalytic antibody (CA) producing
CC bacteriophage. The CAS can be used to activate/deactivate a
CC biological function in an animal by enhancing the rate of cleavage,
CC or formation of a specific bond within a mol. in vivo.
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 47; DB 16; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
IIIIIIIIII
Db 79 LQYASSPYT 87

RESULT 3
AAR80079
ID AAR80079 standard; Protein; 90 AA.

XX
AC AAR80079;
XX
DT 22-MAY-1996 (first entry)
XX
DE Mouse derived light chain RT3 phage antibody pattern C.
XX
KW Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW pattern C.
XX
OS Mus musculus.

XX
FH Key Location/Qualifiers
FT Region 1..15
FT /note= "framework region 1"
FT Region 16..26
FT /note= "complementarity determining region 1"
FT Region 27..40
FT /note= "framework region 2"
FT Region 41..47
FT /note= "complementarity determining region 2"
FT Region 48..78
FT /note= "framework region 3"
FT Region 79..88
FT /note= "complementarity determining region 3"
FT Region 89..90
FT /note= "framework region 4
FT N-terminal fragment"

XX WO9527045-A1.
XX
XX 12-OCT-1995.
XX
XX 30-MAR-1994; 94WO-US03420.
XX
XX 30-MAR-1994; 94WO-US03420.
XX
XX (IGEN-) IGEN INC.
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;

XX WPI; 1995-358624/46.
DR N-PSDB; AAT04626.
XX
PT Production of catalytic antibodies displayed on phage - by
PT generating a gene library of antibody-derived domains and expressing
PT it in phage vectors
XX
PS Disclosure; Fig 9; 133pp; English.
XX
CC AAT04626 encodes AAR80079 mouse derived light chain RT3 phage antibody.
CC The DNA was used in the prepn. of catalytic antibody (CA) producing
CC bacteriophage. The CAs can be used to activate/deactivate a
CC biological function in an animal by enhancing the rate of cleavage,
CC or formation of a specific bond within a mol. in vivo.
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 47; DB 16; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 79 LQYASSPYT 87
|||||

RESULT 4
AAW95480
ID AAW95480 standard; Protein; 92 AA.
XX
AC AAW95480;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW prodrug; scFV.
XX
OS Mus sp.
XX
PN US5855885-A.
XX
PD 05-JAN-1999.
XX
PF 14-JUL-1994; 94US-0273146.
XX
PR 22-JAN-1993; 93US-0007684.
PR 14-JUL-1994; 94US-0273146.
XX
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX
DR WPI; 1999-105036/09.
DR N-PSDB; AAX00879.
XX
PT Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains
PT inserting coding into a phage expression vector and isolating the
PT catalytic antibodies
XX
PS Example 4; Fig 11; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies
CC displayed on a phage. The method comprises: (a) generating a gene library
CC of antibody-derived domains; (b) inserting coding for the domains into a
CC phage expression vector; and (c) isolating the catalytic antibodies. The
CC phage expression vector incorporates a histidine peptide in tandem with a
CC myc peptide. The catalytic antibodies can be isolated by preparing an
CC antigen; optionally immunising an animal with the antigen; generating a
CC library of VH and VL domains from the immunised animal; cloning the VH
CC and VL domains into a phage expression vector to generate phage display
CC antibodies; selecting phage display antibodies which bind specifically
CC to the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a prodrug. The
CC present sequence represents a genetic sequence of light chain PCR
CC pattern C from mouse derived RT3 phage antibodies.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 47; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 81 LQYASSPYT 89
|||||

RESULT 5
AAW95476
ID AAW95476 standard; Protein; 92 AA.
XX
AC AAW95476;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern A genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW prodrug; scFV.
XX
OS Mus sp.
XX
PN US5855885-A.
XX
PD 05-JAN-1999.
XX
PF 14-JUL-1994; 94US-0273146.
XX
PR 22-JAN-1993; 93US-0007684.
PR 14-JUL-1994; 94US-0273146.
XX
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX
DR WPI; 1999-105036/09.
DR N-PSDB; AAX00875.
XX
PT Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains
PT inserting coding into a phage expression vector and isolating the

PT catalytic antibodies
XX
PS Example 4; Fig 9A-F; 117pp; English.
XX
CC The invention relates to methods for producing catalytic antibodies
CC displayed on a phage..The method comprises: (a) generating a gene library
CC of antibody-derived domains; (b) inserting coding for the domains into a
CC phage expression vector; and (c) isolating the catalytic antibodies. The
CC phage expression vector incorporates a histidine peptide in tandem with a
CC myc peptide. The catalytic antibodies can be isolated by preparing an
CC antigen; optionally immunising an animal with the antigen; generating a
CC library of VH and VL domains from the immunised animal; cloning the VH
CC and VL domains into a phage expression vector to generate phage display
CC antibodies; selecting phage display antibodies which bind specifically
CC to the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a prodrug. The
CC present sequence represents a genetic sequence of light chain pattern A
CC from mouse derived RT3 phage antibodies.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 47; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 81 LQYASSPYT 89

RESULT 6
AAW27121
ID AAW27121 standard; Protein; 107 AA.
XX
AC AAW27121;
XX
DT 04-JAN-1998 (first entry)
XX
DE Murine antibody light chain variable region consensus.
XX
KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMFg; tumour; breast cancer; vaccine.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..56
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 88..96
FT /label= CDR3
FT /note= "complementarity determining region 3"
XX
PN WO9722699-A2.
XX
PD 26-JUN-1997.
XX
PF 19-DEC-1996; 96WO-US20757.
XX
PR 13-DEC-1996; 96US-0575762.
PR 20-DEC-1995; 95US-0575762.
PR 26-JAN-1996; 96US-0591965.
XX
PA (KENT) UNIV KENTUCKY.
XX
PI Chatterjee M, Chatterjee SK, Foon KA;
XX

DR WPI; 1997-341690/31.
XX
PT Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
PT against human milk fat globule disease associated tumours,
PT especially breast cancer
XX
PS Example 2; Fig 26C; 130pp; English.
XX
CC This polypeptide sequence comprises a consensus sequence of murine
CC light chain variable regions (VL) selected on the basis of identity
CC to the VL region (see W27119) of monoclonal anti-idiotypic antibody
CC 11D10. The sequences were obtained from a GenBank database
CC search. A VH consensus (W27122) was also produced. 11D10 has at
CC least 18 departures from the consensus sequences (7 in the light
CC chain and 11 in the heavy chain). 8 occur within CDRs and 10
CC outside CDRs. 11D10 polypeptides and polynucleotides can be
CC used in vaccines and pharmaceutical compositions for the treatment
CC of human milk fat globule-associated diseases such as breast
CC cancer.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 47; DB 18; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 89 LQYASSPYT 97

RESULT 7
AAAY44587
ID AAY44587 standard; Protein; 108 AA.
XX
AC AAY44587;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse anti-IL-18 antibody light chain variable region.
XX
KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
KW antiinflammatory; immunosuppressive; leucocytopenic; antialgic;
KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
KW immunopathy; inflammatory disorder; immunoreaction.
XX
OS Mus musculus.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49534.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases
XX
PS Claim 5; Page 17; 36pp; English.
XX
CC The present protein sequence is the mouse anti-Interleukin-18 antibody

CC light chain variable region (VL) encoded by cDNA derived from hybridoma
CC #125-2H. The nucleotide sequence is used in the production of recombinant
CC monoclonal antibody #125-2HmAb, which is capable of neutralising
CC biological activities of interleukin-18. The antibody has antialgic,
CC antiinflammatory, immunosuppressive, leucocytopenic, antipyretic,
CC antiallergic and hepatotropic activity and can be used for prevention and
CC treatment of autoimmune diseases, immunopathies and inflammatory
CC disorders caused by excessive immunoreaction.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 47; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQYASSPYT 9
Db 89 LQYASSPYT 97

RESULT 8
AAV44599
ID AAY44599 standard; Protein; 135 AA.

XX AC AAY44599;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse light chain variable region encoded by PCR A product.
XX
KW Mouse light chain variable region; VL; variable region light chain;
KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
KW hematopoietic; leukocytopenic; antialgic; antipyretic.

OS Mus musculus.
OS Synthetic.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX WPI; 2000-118341/11.
DR N-PSDB; AAZ49548.

XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases .
XX

PS Disclosure; Page 28-29; 32pp; English.

XX
CC The present sequence is the mouse light chain variable region. This was
CC encoded by a recombinant DNA is derived from PCR A which amplifies
CC antibody light chain variable region (VL). The transformant produced
CC using the VL gene was used to transform competent E. coli cells. The peptide
CC produced by transformants neutralises interleukin-18. This is useful for
CC treating and preventing immunopathies, inflammatory disorders and
CC autoimmune diseases which are caused by excessive immunoreaction. The
CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
CC hematopoietic, leukocytopenic, antialgic, antipyretic and hepatic
CC -function improving activities.

XX Sequence 135 AA;

Query Match 100.0%; Score 47; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQYASSPYT 9
Db 109 LQYASSPYT 117

RESULT 9
AAW27119
ID AAW27119 standard; Protein; 145 AA.

XX AC AAW27119;
XX
DT 04-JAN-1998 (first entry)
XX
DE Murine monoclonal anti-idiotypic antibody 11D10 VL region.
XX
KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMFG; tumour; breast cancer; vaccine.
XX
OS Mus musculus.

XX FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Protein 21..145
FT /label= Mat_protein
FT Region 21..43
FT /label= FR1
FT /note= "framework region 1"
FT Region 44..54
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 55..69
FT /label= FR2
FT /note= "framework region 2"
FT Region 70..76
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 77..108
FT /label= FR3
FT /note= "framework region 3"
FT Region 109..117
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT Region 118..127
FT /label= FR1
FT /note= "framework region 4"

XX WO9722699-A2.

XX 26-JUN-1997.

PF 19-DEC-1996; 96WO-US20757.

PR 13-DEC-1996; 96US-0575762.

PR 20-DEC-1995; 95US-0575762.

PR 26-JAN-1996; 96US-0591965.

XX (KENT) UNIV KENTUCKY.

XX Chatterjee M, Chatterjee SK, Foon KA;

XX WPI; 1997-341690/31.

DR N-PSDB; AAT85149.

XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
PT against human milk fat globule disease associated tumours,
PT especially breast cancer
XX

PS Claim 9; Page 94; 130pp; English.

XX This polypeptide sequence comprises the light chain variable region

CC (VL) of monoclonal anti-idiotypic antibody 11D10 produced by

CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising

CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic

CC response. It elicits an immune response against a specific epitope

CC of a high mol.wt. mucin of human milk fat globule (HMFG). It

CC induces an immunological response to HMFG in mice, rabbits, monkeys

CC and patients with advanced HMFG-associated tumours. Pharmaceutical

CC compositions and vaccines comprising 11D10, 11D10 polypeptides

CC and/or 11D10 polynucleotides (see also AAT85149-50) are claimed.

CC Also claimed are diagnostic kits and methods of using 11D10, 11D10

CC polypeptides and/or 11D10 polynucleotides, including methods of

CC treating HMFG-associated tumours. 11D10 is also used in a claimed

CC method of palliating HMFG-associated disease and in claimed kits to

CC detect or quantify anti-HMFG antibody.

XX

SQ Sequence 145 AA;

Query Match 100.0%; Score 47; DB 18; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9

Db 109 LQYASSPYT 117

RESULT 10

AAW87593

ID AAW87593 standard; Protein; 145 AA.

XX

AC AAW87593;

XX

DT 16-MAR-1999 (first entry)

XX

DE Antibody 11D10 light chain variable region.

XX

KW Murine; mouse; antibody; light chain; variable region; anti-idiotypic;

KW human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Peptide 1..20

FT /note= "signal peptide"

FT Protein 21..999

FT /note= "mature protein"

FT Region 21..43

FT /label= framework_1

FT Domain 44..54

FT /label= CDR1

FT /note= "complementarity determining region 1"

FT Region 55..69

FT /label= framework_2

FT Misc-difference 55

FT /note= "encoded by TGG"

FT Domain 70..76

FT /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 77..108

FT /label= framework_3

FT Domain 109..117

FT /label= CDR3

FT /note= "complementarity determining region 3"

FT Region 118..127

FT /label= framework_4

XX

PN W09856419-A1.

XX

PD 17-DEC-1998.

XX

PF 12-JUN-1998; 98WO-US12250.

XX

PR 11-JUN-1998; 98US-0096244.

PR 13-JUN-1997; 97US-0049540.

XX

PA (KENT) UNIV KENTUCKY RES FOUND.

XX

PI Chatterjee M, Foon KA;

XX

DR WPI; 1999-060029/05.

DR N-PSDB; AAV83772.

XX

PT Delaying development of, or treating, HMFG-associated tumours -

PT using anti-idiotypic antibody 11D10 raised against antibodies to

PT human milk fat globule protein

XX

PS Disclosure; Fig 1; 54pp; English.

XX

CC This sequence represents the light chain variable region of the murine

CC antibody 11D10. This anti-idiotypic antibody is used to delay the

CC development of, or treat, a human milk fat globule (HMFG) associated

CC tumour in an individual having low tumour burden. The antibody 11D10

CC is used to prevent the recurrence of HMFG-associated tumours e.g.

CC ovarian, non-small cell lung and pancreatic carcinoma, especially for

CC treating breast tumours.

XX

SQ Sequence 145 AA;

Query Match 100.0%; Score 47; DB 20; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9

Db 109 LQYASSPYT 117

RESULT 11

AAW44595

ID AAY44595 standard; Protein; 237 AA.

XX

AC AAY44595;

XX

DT 04-APR-2000 (first entry)

XX

DE EscFv#125-2H recombinant protein.

XX

KW EscFv#125-2H recombinant protein; interleukin-18; mouse;

KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;

KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;

KW antialgic; antipyretic.

XX

OS Mus musculus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Domain 1..113

FT /note= "Heavy chain variable region"

FT Domain 114..130

FT /note= "Glycine-serine linker"

FT Domain 131..237

FT /note= "Light chain variable region"

XX

PN EP974600-A2.

XX

PD 26-JAN-2000.

XX

PF 24-JUN-1999; 99EP-0304977.

XX

PR 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.

PR 22-DEC-1998; 98JP-0365023.

XX

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49542.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 8; Page 19-20; 32pp; English.
XX
CC The present sequence is EscFv#125-2H protein encoded by recombinant cDNA
CC pEscFv#125-2H for neutralising interleukin-18. The protein is produced
CC from hybridoma #125-2H by transforming pEscFv#125-2H in competent
CC E. coli cells. This is useful for treating and preventing immunopathies,
CC inflammatory disorders and autoimmune diseases which are caused by
CC excessive immunoreaction. The protein has anti-allergic,
CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,
CC antialgic, antipyretic and hepatic-function improving activities.
XX
SQ Sequence 237 AA;

Query Match 100.0%; Score 47; DB 21; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 219 LQYASSPYT 227
| | | | | | | | | |

RESULT 12
AA44596
ID AAY44596 standard; Protein; 243 AA.
XX
AC AAY44596;
XX
DT 04-APR-2000 (first entry)
XX
DE EscFv#125-2H.HT recombinant protein.
XX
KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49543.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 8; Page 20-21; 32pp; English.
XX
CC The present sequence is EscFv#125-2H.HT protein encoded by
CC recombinant cDNA pEscFv#125-2H.HT for neutralising interleukin-18. The
CC protein is produced from hybridoma #125-2H by transforming
CC pEscFv#125-2H.HT in competent E. coli cells. There are six histidine
CC residues positioned after the light chain variable region. This protein
CC is useful for treating and preventing immunopathies, inflammatory
CC disorders and autoimmune diseases which are caused by excessive
CC immunoreaction. The protein has anti-allergic, anti-inflammatory,
CC immunosuppressive, hematopoietic, leukocytopoietic, antialgic,
CC antipyretic and hepatic-function improving activities.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 47; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 219 LQYASSPYT 227
| | | | | | | | | |

RESULT 13
AAU72863
ID AAU72863 standard; Protein; 252 AA.
XX
AC AAU72863;
XX
DT 26-FEB-2002 (first entry)
XX
DE P4-14 single chain Fv.
XX
KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
XX
OS Homo sapiens.
XX
PN WO200171005-A2.
XX
PD 27-SEP-2001.
XX
PF 26-MAR-2001; 2001WO-EP03414.
XX
PR 24-MAR-2000; 2000EP-0106467.
XX
PA (KUFE/) KUFE P.
XX
PI Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Mischel R;
PI Mayer M, Hofmeister R;
XX
DR WPI; 2002-055119/07.
DR N-PSDB; AAS97137.
XX
PT Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -

XX Example 7; Fig 16; 114pp; English.
PS
XX
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
XX receptor and the polypeptides of the invention.
SQ Sequence 252 AA;

Query Match 100.0%; Score 47; DB 23; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQYASSPYT 9
Db 222 LQYASSPYT 230

RESULT 14
AAU72869
ID AAU72869 standard; Protein; 257 AA.
XX
AC AAU72869;

26-FEB-2002 (first entry)
P5-11 single chain Fv.

XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

XX Homo sapiens.
OS
XX
PN WO200171005-A2.
XX
PD 27-SEP-2001.

26-MAR-2001; 2001WO-EP03414.

24-MAR-2000; 2000EP-0106467.

(KUFE/) KUFER P.

XX Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;

XX WPI; 2002-055119/07.
DR N-PSDB; AAS97143.

XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating

PT cancers and infectious diseases -
XX Example 7; Fig 16; 114pp; English.
PS
XX
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
XX receptor and the polypeptides of the invention.
SQ Sequence 257 AA;

Query Match 100.0%; Score 47; DB 23; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQYASSPYT 9
Db 227 LQYASSPYT 235

RESULT 15
AAU72872
ID AAU72872 standard; Protein; 499 AA.
XX
AC AAU72872;

26-FEB-2002 (first entry)

3B10xP4-14 bispecific single chain Fv.

XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

XX Homo sapiens.

PN WO200171005-A2.

27-SEP-2001.

26-MAR-2001; 2001WO-EP03414.

24-MAR-2000; 2000EP-0106467.

(KUFE/) KUFER P.

XX Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;

XX WPI; 2002-055119/07.
DR N-PSDB; AAS97146.

XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and

PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
XX
PS Example 5; Fig 16; 114pp; English.
XX
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
CC receptor and the polypeptides of the invention.
XX
SQ Sequence 499 AA;

Query Match 100.0%; Score 47; DB 23; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
 | | | | | | | | | |
Db 469 LQYASSPYT 477

Search completed: March 10, 2003, 16:56:56
Job time : 25.4483 secs

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OM protein - protein search, using sw model
Run on: March 10, 2003, 16:46:26 ; Search time 24.2759 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				%		Query		Match		Length		DB		ID		Description	
Result No.	Score	Score	Match	Match	Length	Length	DB	DB	ID	ID	ID	ID	ID	ID	ID	ID	Description
1	38	70.4	127	11	Q925S9	Q925S9	mus	musculu	Q925S9	mus	musculu	Q925S9	mus	musculu	Q925S9	mus	musculu
2	37	68.5	479	15	Q84808	Q84808	puma	lentiv	Q84808	puma	lentiv	Q84808	puma	lentiv	Q84808	puma	lentiv
3	36	66.7	293	12	Q80851	Q80851	hydrangea	m	Q80851	hydrangea	m	Q80851	hydrangea	m	Q80851	hydrangea	m
4	36	66.7	305	16	Q8ZDQ5	Q8ZDQ5	yersinia	pe	Q8ZDQ5	yersinia	pe	Q8ZDQ5	yersinia	pe	Q8ZDQ5	yersinia	pe
5	36	66.7	442	16	Q84377	Q84377	chlamydia	t	Q84377	chlamydia	t	Q84377	chlamydia	t	Q84377	chlamydia	t
6	36	66.7	548	10	Q9C6L8	Q9C6L8	arabidopsis		Q9C6L8	arabidopsis		Q9C6L8	arabidopsis		Q9C6L8	arabidopsis	
7	35	64.8	194	3	Q93950	Q93950	candida	alb	Q93950	candida	alb	Q93950	candida	alb	Q93950	candida	alb
8	35	64.8	211	2	Q9F8M9	Q9F8M9	carboxydoth		Q9F8M9	carboxydoth		Q9F8M9	carboxydoth		Q9F8M9	carboxydoth	
9	35	64.8	219	11	Q9Q261	Q9Q261	mus	musculu	Q9Q261	mus	musculu	Q9Q261	mus	musculu	Q9Q261	mus	musculu
10	35	64.8	231	11	Q9WUI0	Q9WUI0	mus	musculu	Q9WUI0	mus	musculu	Q9WUI0	mus	musculu	Q9WUI0	mus	musculu
11	35	64.8	232	4	Q9H2W2	Q9H2W2	homo	sapien	Q9H2W2	homo	sapien	Q9H2W2	homo	sapien	Q9H2W2	homo	sapien
12	34	63.0	45	2	Q9ZG20	Q9ZG20	chlamydia	t	Q9ZG20	chlamydia	t	Q9ZG20	chlamydia	t	Q9ZG20	chlamydia	t
13	34	63.0	160	17	Q8U198	Q8U198	pyrococcus		Q8U198	pyrococcus		Q8U198	pyrococcus		Q8U198	pyrococcus	
14	34	63.0	193	16	Q9JWK5	Q9JWK5	neisseria	m	Q9JWK5	neisseria	m	Q9JWK5	neisseria	m	Q9JWK5	neisseria	m
15	34	63.0	216	13	Q9PU79	Q9PU79	crocodylus		Q9PU79	crocodylus		Q9PU79	crocodylus		Q9PU79	crocodylus	
16	34	63.0	269	16	O51586	O51586	borrelia	bu	O51586	borrelia	bu	O51586	borrelia	bu	O51586	borrelia	bu

17	34	63.0	285	10	Q41176	Q41176	luffa	cylin	Q41176	luffa	cylin	Q41176	luffa	cylin	Q41176	luffa	cylin
18	34	63.0	324	16	Q828X4	Q828X4	salmonella		Q828X4	salmonella		Q828X4	salmonella		Q828X4	salmonella	
19	34	63.0	330	10	Q94JY0	Q94JY0	arabidopsis		Q94JY0	arabidopsis		Q94JY0	arabidopsis		Q94JY0	arabidopsis	
20	34	63.0	377	10	Q49495	Q49495	arabidopsis		Q49495	arabidopsis		Q49495	arabidopsis		Q49495	arabidopsis	
21	34	63.0	471	16	Q9PK22	Q9PK22	chlamydia	m	Q9PK22	chlamydia	m	Q9PK22	chlamydia	m	Q9PK22	chlamydia	m
22	34	63.0	494	2	Q9AFS3	Q9AFS3	shigella	fl	Q9AFS3	shigella	fl	Q9AFS3	shigella	fl	Q9AFS3	shigella	fl
23	34	63.0	494	2	Q8VSH5	Q8VSH5	shigella	fl	Q8VSH5	shigella	fl	Q8VSH5	shigella	fl	Q8VSH5	shigella	fl
24	34	63.0	525	4	Q96N21	Q96N21	homo	sapien	Q96N21	homo	sapien	Q96N21	homo	sapien	Q96N21	homo	sapien
25	34	63.0	536	3	Q9UVS8	Q9UVS8	aspergillus		Q9UVS8	aspergillus		Q9UVS8	aspergillus		Q9UVS8	aspergillus	
26	34	63.0	565	16	Q8XJE4	Q8XJE4	clostridium		Q8XJE4	clostridium		Q8XJE4	clostridium		Q8XJE4	clostridium	
27	34	63.0	610	2	Q93G04	Q93G04	lactobacilli		Q93G04	lactobacilli		Q93G04	lactobacilli		Q93G04	lactobacilli	
28	34	63.0	644	16	Q98CV7	Q98CV7	rhizobium	l	Q98CV7	rhizobium	l	Q98CV7	rhizobium	l	Q98CV7	rhizobium	l
29	34	63.0	799	2	Q8RKZ1	Q8RKZ1	providencia		Q8RKZ1	providencia		Q8RKZ1	providencia		Q8RKZ1	providencia	
30	34	63.0	886	16	Q9CBY7	Q9CBY7	mycobacteri		Q9CBY7	mycobacteri		Q9CBY7	mycobacteri		Q9CBY7	mycobacteri	
31	33.5	62.0	370	5	Q8SUY4	Q8SUY4	encephalito		Q8SUY4	encephalito		Q8SUY4	encephalito		Q8SUY4	encephalito	
32	33	61.1	184	11	Q9DAR5	Q9DAR5	mus	musculu	Q9DAR5	mus	musculu	Q9DAR5	mus	musculu	Q9DAR5	mus	musculu
33	33	61.1	216	13	Q9PU23	Q9PU23	trachemys	s	Q9PU23	trachemys	s	Q9PU23	trachemys	s	Q9PU23	trachemys	s
34	33	61.1	225	2	Q68118	Q68118	rhodobacter		Q68118	rhodobacter		Q68118	rhodobacter		Q68118	rhodobacter	
35	33	61.1	237	3	Q08914	Q08914	saccharomyc		Q08914	saccharomyc		Q08914	saccharomyc		Q08914	saccharomyc	
36	33	61.1	237	3	Q08992	Q08992	saccharomyc		Q08992	saccharomyc		Q08992	saccharomyc		Q08992	saccharomyc	
37	33	61.1	245	12	Q9QKC4	Q9QKC4	rift	valley	Q9QKC4	rift	valley	Q9QKC4	rift	valley	Q9QKC4	rift	valley
38	33	61.1	246	12	Q9QKC5	Q9QKC5	triticum	ae	Q9QKC5	triticum	ae	Q9QKC5	triticum	ae	Q9QKC5	triticum	ae
39	33	61.1	312	10	Q8W0W8	Q8W0W8	triticum	ae	Q8W0W8	triticum	ae	Q8W0W8	triticum	ae	Q8W0W8	triticum	ae
40	33	61.1	312	16	Q8XM31	Q8XM31	clostridium		Q8XM31	clostridium		Q8XM31	clostridium		Q8XM31	clostridium	
41	33	61.1	314	11	Q8VGN1	Q8VGN1	mus	musculu	Q8VGN1	mus	musculu	Q8VGN1	mus	musculu	Q8VGN1	mus	musculu
42	33	61.1	334	10	Q9LUW3	Q9LUW3	arabidopsis		Q9LUW3	arabidopsis		Q9LUW3	arabidopsis		Q9LUW3	arabidopsis	
43	33	61.1	346	16	O86705	O86705	streptomyce		O86705	streptomyce		O86705	streptomyce		O86705	streptomyce	
44	33	61.1	349	16	Q9RUY4	Q9RUY4	deinococcus		Q9RUY4	deinococcus		Q9RUY4	deinococcus		Q9RUY4	deinococcus	
45	33	61.1	366	16	Q92WQ5	Q92WQ5	rhizobium	m	Q92WQ5	rhizobium	m	Q92WQ5	rhizobium	m	Q92WQ5	rhizobium	m

ALIGNMENTS

RESULT 1

Q925S9 PRELIMINARY; PRT; 127 AA.
AC Q925S9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Immunoglobulin light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=99306687; PubMed=10380019;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA Foon K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotypic antibody mimicking a breast cancer-
RT associated antigen and the cytokine GM-CSF.";
RL Hybridoma 18:193-202(1999).
DR EMBL; AF124721; AAK55120.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 127 127
SQ SEQUENCE 127 AA; 13794 MW; 13F61BEBBB981FA5 CRC64;

Query Match 70.4%; Score 38; DB 11; Length 127;
Best Local Similarity 72.7%; Pred. NO. 5.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
Db 44 RASQDIGINLH 54

RESULT 2
Q84808

ID	Q84808	PRELIMINARY;	PRT;	479 AA.
AC	Q84808;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	GAG polyprotein [Contains: core protein(s) p24].			
GN	GAG.			
OS	puma lentivirus 14.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=32615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94303200; PubMed=8030248;			
RA	Langley R.J., Hirsch V.M., O'Brien S.J., Adger-Johnson D.,			
RA	Goeken R.M., Olmsted R.A.;			
RT	"Nucleotide sequence analysis of puma lentivirus (PLV-14): genomic			
RT	organization and relationship to other lentiviruses.";			
RL	Virology 202:853-864(1994).			
CC	-!- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).			
DR	EMBL; U03982; AAA67167.1; -.			
DR	HSSP; P03351; 1E1A.			
DR	InterPro; IPR000721; Gag_p24.			
DR	InterPro; IPR001878; Znf_CCHC.			
DR	Pfam; PF00607; Gag_p24; 1.			
DR	Pfam; PF00098; zf-CCHC; 2.			
DR	PRINTS; PR00939; C2HC2NFINGER.			
DR	SMART; SM00343; Znf_C2HC; 2.			
KW	Core protein; Polyprotein.			
SQ	SEQUENCE 479 AA; 52647 MW; 21C4190013B21242 CRC64;			
Query Match 68.5%; Score 37; DB 15; Length 479;				
Best Local Similarity 72.7%; Pred. No. 39;				
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 RASQDIGSKLY 11			
Db	343 RACQDIGSTQY 353			
RESULT 3				
ID	Q80851	PRELIMINARY;	PRT;	293 AA.
AC	Q80851;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	3a protein.			
OS	hydrangea mosaic virus.			
OC	viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;			
OC	ilarvirus.			
OX	NCBI_TaxID=42812;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96290233; PubMed=8725121;			
RA	Ge X., Scott S.W.;			
RT	"The nucleotide sequence of hydrangea mosaic virus RNA 3 exhibits			
RT	similarity with the RNA 3 of tobacco streak virus.";			
RL	Virus Res. 40:57-63(1996).			
DR	EMBL; U35145; AAA80344.1; -.			
DR	InterPro; IPR002538; Bromo_MP.			
DR	Pfam; PF01573; Bromo_MP; 1.			
SQ	SEQUENCE 293 AA; 32112 MW; 734612E4A1934A75 CRC64;			
Query Match 66.7%; Score 36; DB 12; Length 293;				
Best Local Similarity 72.7%; Pred. No. 37;				
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 RASQDIGSKLY 11			
Db	213 RASTDIASKRY 223			
RESULT 4				

Q8ZDQ5				
ID	Q8ZDQ5	PRELIMINARY;	PRT;	305 AA.
AC	Q8ZDQ5;			
DT	01-MAR-2002	(TREMBLrel. 20, Created)		
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Sugar binding protein.			
GN	RBSB OR YPO2501.			
OS	Yersinia pestis.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Yersinia.			
OX	NCBI_TaxID=632;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CO-92 / BIOVAR ORIENTALIS;			
RX	MEDLINE=21470413; PubMed=11586360;			
RA	Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,			
RA	Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,			
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,			
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,			
RA	Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,			
RA	Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,			
RA	Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;			
RT	"Genome sequence of Yersinia pestis, the causative agent of plague.";			
RL	Nature 413:523-527(2001).			
DR	EMBL; AJ414152; CAC91306.1; -.			
DR	InterPro; IPR001761; PeriplaBP/LacI.			
DR	Pfam; PF00532; Peripla_BP_like; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 305 AA; 32433 MW; 148AD7DDE3FF559B CRC64;			
Query Match 66.7%; Score 36; DB 16; Length 305;				
Best Local Similarity 54.5%; Pred. No. 38;				
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;				
QY	1 RASQDIGSKLY 11			
	: : : :			
Db	52 QAANDIGAKVY 62			
RESULT 5				
ID	O84377	PRELIMINARY;	PRT;	442 AA.
AC	O84377;			
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	Hypothetical protein CT372.			
GN	CT372.			
OS	Chlamydia trachomatis.			
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.			
OX	NCBI_TaxID=813;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=D/UW-3/CX;			
RX	MEDLINE=99000809; PubMed=9784136;			
RA	Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,			
RA	Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,			
RA	Davis R.W.;			
RT	"Genome sequence of an obligate intracellular pathogen of humans:			
RT	Chlamydia trachomatis.";			
RL	Science 282:754-759(1998).			
DR	EMBL; AE001310; AAC67968.1; -.			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 442 AA; 49399 MW; 12DF52703A827408 CRC64;			
Query Match 66.7%; Score 36; DB 16; Length 442;				
Best Local Similarity 80.0%; Pred. No. 58;				
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	2 ASQDIGSKLY 11			
Db	327 ASQHISSKLY 336			

SQ SEQUENCE 194 AA; 22307 MW; F119E1A0A250F7B1 CRC64;									
Query Match 64.8%; Score 35; DB 3; Length 194;									
Best Local Similarity 77.8%; Pred. No. 37;									
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	3	SQDIGSKLY 11							
Db	46	SQDFGSKLY 54							
RESULT 8									
Q9F8M9 PRELIMINARY; PRT; 211 AA.									
ID	Q9F8M9;								
DT	01-MAR-2001	(TrEMBLrel. 16, Created)							
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)							
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)							
DE	4-hydroxybutyrate CoA transferase (Fragment).								
OS	Carboxydothermus hydrogenoformans.								
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;								
OC	Clostridiales; Peptococcaceae; Carboxydothermus.								
OX	NCBI_TaxID=129958;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Gonzalez J.M., Robb F.T.;								
RT	"A genomic survey of the extreme thermophilic, CO-utilizing bacterium								
RT	Carboxydothermus hydrogenoformans.";								
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AF244604; AAG23553.1; -.								
DR	InterPro; IPR003702; AcetylCoA_hydro.								
DR	Pfam; PF02550; AcetylCoA_hydro; 1.								
KW	Transferase.								
FT	NON_TER	1	1						
FT	NON_TER	211	211						
SQ	SEQUENCE	211 AA; 23149 MW; C3038601E0C79E82	CRC64;						
Query Match 64.8%; Score 35; DB 2; Length 211;									
Best Local Similarity 60.0%; Pred. No. 41;									
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;									
QY	2	ASQDIGSKLY 11							
Db	183	ASESIGTKIY 192							
RESULT 9									
Q9QZ61 PRELIMINARY; PRT; 219 AA.									
ID	Q9QZ61;								
AC	Q9QZ61;								
DT	01-MAY-2000	(TrEMBLrel. 13, Created)							
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)							
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)							
DE	Mix-related homeobox protein (Fragment).								
GN	MIXL1.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Yu Y., Chen S.W., Gudas L.J.;								
RT	"mMix, a Mouse Mix-related Homeobox Gene Expressed in the Primitive								
RT	Streak.";								
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.								
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).								
DR	EMBL; AF201959; AAF08314.1; -.								
DR	HSSP; P06601; 1FJL.								
DR	MGD; MGI:1351322; Mixl1.								
DR	InterPro; IPR001356; Homeobox.								
DR	Pfam; PF00046; homeobox; 1.								
DR	ProDom; PD000010; Homeobox; 1.								
DR	SMART; SM00389; HOX; 1.								
FT	NON_TER	1	1						

SQ SEQUENCE 548 AA; 61719 MW; ACB3B0F801D27518 CRC64;									
Query Match 66.7%; Score 36; DB 10; Length 548;									
Best Local Similarity 63.6%; Pred. No. 74;									
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;									
QY	1	RASQDIGSKLY 11							
Db	48	KALYDIGAKLY 58							
RESULT 7									
O93950 PRELIMINARY; PRT; 194 AA.									
ID	O93950;								
AC	O93950;								
DT	01-MAY-1999	(TrEMBLrel. 10, Created)							
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)							
DT	01-MAY-1999	(TrEMBLrel. 10, Last annotation update)							
DE	CTA6p (Fragment).								
GN	CTA6.								
OS	Candida albicans (Yeast).								
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;								
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.								
OX	NCBI_TaxID=5476;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Kaiser B., Kunkel W., Saluz H.P., Munder T.;								
RT	"Identification of Candida albicans protein domains with								
RT	transcriptional activating properties in Saccharomyces cerevisiae.";								
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AJ006641; CAA07169.1; -.								
FT	NON_TER	1	1						

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DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 219 AA; 23639 MW; BD729DF8F1C8D1C3 CRC64;

Query Match 64.8%; Score 35; DB 11; Length 219;
Best Local Similarity 87.5%; Pred. NO. 43;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
   |:|||||
Db 198 SEDIGSKL 205

RESULT 10
Q9WUI0
ID Q9WUI0 PRELIMINARY; PRT; 231 AA.
AC Q9WUI0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mix-like homeobox protein (Homeobox protein MIX).
GN MIXL1 OR MML OR MIX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425184; PubMed=10495285;
RA Pearce J.J., Evans M.J.;
RT "Mml, a mouse mix-like gene expressed in the primitive streak.";
RL Mech. Dev. 87:189-192(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=EMBRYO;
RA Robb L., Hartley L., Begley C.G., Elefanty A.G.;
RT "Expression of the homeobox gene mMix is restricted to the primitive
RT streak of the gastrulating mouse embryo.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF135063; AAD25543.1; -.
DR EMBL; AF154573; AAK59867.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04800; -.
DR MGD; MGI:1351322; Mixl1.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 231 AA; 24844 MW; 59DA80A5E7E6EE33 CRC64;

Query Match 64.8%; Score 35; DB 11; Length 231;
Best Local Similarity 87.5%; Pred. NO. 45;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
   |:|||||
Db 210 SEDIGSKL 217

RESULT 11
Q9H2W2
ID Q9H2W2 PRELIMINARY; PRT; 232 AA.
AC Q9H2W2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mix-like homeobox protein 1 (Homeodomain protein MIX).
```

```
GN MILD1 OR MIX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Guo W., Nagarajan L.;
RT "MILD1, a human mix.1-like gene.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Robb L.G., Hartley L., Stanley E.G., Begley C.G., Brodnicki T.C.,
RA Copeland N.G., Gilbert D.J., Jenkins N.A., Elefanty A.G.;
RT "Mix, a murine homolog of the Xenopus Mix.1 gene, is expressed in the
RT presumptive posterior region of the prestreak embryo and in the
RT primitive streak.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF211891; AAG35776.1; -.
DR EMBL; AF218357; AAK01479.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04801; -.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 232 AA; 24659 MW; 2E8A6A811799A8F0 CRC64;

Query Match 64.8%; Score 35; DB 4; Length 232;
Best Local Similarity 87.5%; Pred. NO. 46;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
   |:|||||
Db 211 SEDIGSKL 218

RESULT 12
Q9ZG20
ID Q9ZG20 PRELIMINARY; PRT; 45 AA.
AC Q9ZG20;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Procarboxypeptidase A complex component III (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
RT sequencing.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087356; AAD04128.1; -.
KW Carboxypeptidase.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5067 MW; FC99367724DF12F8 CRC64;

Query Match 63.0%; Score 34; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. NO. 12;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
   ||| | |||
Db 9 ASQYISSKLY 18
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RESULT 13
Q8U198
ID Q8U198 PRELIMINARY; PRT; 160 AA.
AC Q8U198;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein PFI324.
GN PFI324.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010237; AAL81448.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 160 AA; 18742 MW; 7E3B496DC037A79F CRC64;

Query Match 63.0%; Score 34; DB 17; Length 160;
Best Local Similarity 45.5%; Pred. No. 49;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
| :|:| | :|
Db 89 RKAQELGKKIY 99

RESULT 14
Q9JWK5
ID Q9JWK5 PRELIMINARY; PRT; 193 AA.
AC Q9JWK5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein NMA0330.
GN NMA0330.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162752; CAB83635.1; -.
DR InterPro; IPR002698; FTHF_cligase.
DR Pfam; PF01812; 5-FTHF_cyc-lig; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 193 AA; 22211 MW; 7A12CE166600B27F CRC64;

Query Match 63.0%; Score 34; DB 16; Length 193;
Best Local Similarity 63.6%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
| :|:| | :|
Db 63 RAAQKRGAKLY 73
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RESULT 15
Q9PU79
ID Q9PU79 PRELIMINARY; PRT; 216 AA.
AC Q9PU79;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Pyruvate kinase (EC 2.7.1.40) (PK) (Fragment).
OS Crocodylus niloticus (Nile crocodile) (African crocodile).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Crocodylinae; Crocodylus.
OX NCBI_TaxID=8501;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20022983; PubMed=10555283;
RA Hughes S., Zelus D., Mouchiroud D.;
RT "Warm-blooded isochore structure in Nile crocodile and turtle.";
RL Mol. Biol. Evol. 16:1521-1527(1999).
CC -|- CATALYTIC ACTIVITY: ATP + PYRUVATE -> ADP + PHOSPHOENOLPYRUVATE.
CC -|- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM (BY SIMILARITY).
CC -|- PATHWAY: FINAL STEP IN GLYCOLYSIS.
CC -|- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
DR EMBL; AJ011395; CAB56421.1; -.
DR HSSP; P11974; 1AQF.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF00224; PK; 1.
DR PRINTS; PR01050; PYRUVTKNASE.
DR ProDom; PD001009; Pyruvate_kinase; 1.
DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
KW Glycolysis; Kinase; Magnesium; Transferase.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23509 MW; 5FCF3CEC2BDB5074 CRC64;

Query Match 63.0%; Score 34; DB 13; Length 216;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DIGSKLY 11
| :|:| | :|
Db 45 DIGSKIY 51

Search completed: March 10, 2003, 17:00:06
Job time : 26.2759 secs
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GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 10, 2003, 16:46:26 ; Search time 15.4483 Seconds
(without alignments)
93.365 Million cell updates/sec
Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSSLDS 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	100.0	131	16	Q92IW9	Q92iw9 rickettsia
2	31	100.0	320	16	Q8YEY4	Q8yey4 brucella me
3	31	100.0	548	16	Q9ZDV5	Q9zdv5 rickettsia
4	31	100.0	565	9	Q9MBU6	Q9mbu6 chlamydia p
5	31	100.0	589	16	O06967	O06967 bacillus su
6	31	100.0	589	16	Q92IY4	Q92iy4 rickettsia
7	31	100.0	596	2	Q9L7X7	Q9l7x7 brucella ab
8	31	100.0	600	16	Q8U6S8	Q8u6s8 agrobacteri
9	31	100.0	601	16	Q98LY9	Q98ly9 rhizobium l
10	31	100.0	604	16	Q52924	Q52924 rhizobium m
11	31	100.0	606	5	Q9W0C5	Q9w0c5 drosophila
12	31	100.0	631	16	Q98AT0	Q98at0 rhizobium l
13	31	100.0	947	5	Q08667	Q08667 plasmodium
14	31	100.0	1025	5	Q25693	Q25693 plasmodium
15	31	100.0	1415	5	Q9NG76	Q9ng76 plasmodium
16	29	93.5	612	5	Q962H4	Q962h4 encephalito

17	29	93.5	1552	5	Q9VUE8	Q9vue8 drosophila
18	28	90.3	43	3	Q9URF0	Q9urf0 saccharomyc
19	28	90.3	85	2	Q54733	Q54733 synechococc
20	28	90.3	111	3	Q05453	Q05453 saccharomyc
21	28	90.3	149	5	Q9Y0C3	Q9y0c3 mytilus edu
22	28	90.3	255	10	Q9FFM7	Q9ffm7 arabidopsis
23	28	90.3	289	5	Q9VG0	Q9vgv0 drosophila
24	28	90.3	301	5	Q9NKY3	Q9nky3 physarum po
25	28	90.3	327	2	O30552	O30552 helicobacte
26	28	90.3	327	16	O26096	O26096 helicobacte
27	28	90.3	327	16	Q9ZJ34	Q9zj34 helicobacte
28	28	90.3	351	2	Q93K83	Q93k83 escherichia
29	28	90.3	387	16	Q9ACT1	Q9act1 streptomyc
30	28	90.3	469	4	O14573	O14573 homo sapien
31	28	90.3	534	16	P73533	P73533 synechocyst
32	28	90.3	546	16	Q8YZ47	Q8yz47 anabaena sp
33	28	90.3	564	16	Q8REL9	Q8rel9 fusobacteri
34	28	90.3	565	5	Q9BL17	Q9bl17 caenorhabdi
35	28	90.3	571	2	Q54121	Q54121 staphylococ
36	28	90.3	575	16	Q927A1	Q927a1 listeria in
37	28	90.3	575	16	Q8Y3T6	Q8y3t6 listeria mo
38	28	90.3	578	16	Q9KEY6	Q9key6 bacillus ha
39	28	90.3	583	2	O32748	O32748 lactobacill
40	28	90.3	583	16	Q8RFT9	Q8rft9 fusobacteri
41	28	90.3	587	5	Q9U7F4	Q9u7f4 onchocerca
42	28	90.3	587	16	Q99YA5	Q99ya5 streptococc
43	28	90.3	587	16	Q8U754	Q8u754 agrobacteri
44	28	90.3	588	16	Q9RRV6	Q9rrv6 deinococcus
45	28	90.3	592	16	Q8Y258	Q8y258 ralstonia s

ALIGNMENTS

RESULT 1

Q92IW9 ID Q92IW9 PRELIMINARY; PRT; 131 AA.
AC Q92IW9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN RC0301.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008596; AAL02839.1; -.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR proDom; PD000006; ABC_transportr; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 131 AA; 14753 MW; C8484BCCA612872D CRC64;

Query Match 100.0%; Score 31; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLDS 7
Db 62 ATSSSLDS 68

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RESULT 2
Q8YEY4
ID Q8YEY4 PRELIMINARY; PRT; 320 AA.
AC Q8YEY4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC transporter ATP-binding protein.
GN BMEI1743.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009607; AAL52924.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Complete proteome.
SQ SEQUENCE 320 AA; 35768 MW; 95DBAB38430A2C01 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 320;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 235 ATSSLDS 241

RESULT 3
Q9ZDV5
ID Q9ZDV5 PRELIMINARY; PRT; 548 AA.
AC Q9ZDV5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC transporter ATP-binding protein (ABCT3).
GN RP214.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
DR EMBL; AJ235270; CAA14677.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportrTM.
DR InterPro; IPR003439; ABC_transportr.
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DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 548 AA; 62589 MW; B4ED4E7F9D53EDC9 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 548;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 470 ATSSLDS 476

RESULT 4
Q9MBU6
ID Q9MBU6 PRELIMINARY; PRT; 565 AA.
AC Q9MBU6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Structural protein.
GN VP1.
OS Chlamydia phage 2.
OC Viruses; ssDNA viruses; Microviridae; Chlamydia microvirus.
OX NCBI_TaxID=105154;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193783; PubMed=10729119;
RA Liu B., Everson J.S., Fane B., Giannikopoulou P., Vretou E.,
RA Lambden P.R., Clarke I.N.;
RT "Molecular characterisation of a bacteriophage (Chp2) from Chlamydia
RT psittaci.";
RL J. Virol. 74:3464-3469(2000).
DR EMBL; AJ270057; CAB85589.1; -.
SQ SEQUENCE 565 AA; 63538 MW; 670485CDC2A94932 CRC64;

Query Match 100.0%; Score 31; DB 9; Length 565;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 497 ATSSLDS 503

RESULT 5
O06967
ID O06967 PRELIMINARY; PRT; 589 AA.
AC O06967;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein yvcc.
GN yvcc.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Denizot F.C.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
```



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RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kilaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
   (ABC TRANSPORTERS).
DR EMBL; Z94043; CAB08051.1; -.
DR EMBL; Z99121; CAB15487.1; -.
DR HSSP; P13569; 1NBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Hypothetical protein; Transport; Complete proteome.
SQ SEQUENCE 589 AA; 64519 MW; 8A15163B5698DA08 CRC64;

  Query Match          100.0%; Score 31; DB 16; Length 589;
  Best Local Similarity 100.0%; Pred. No. 37;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 505 ATSSLDS 511
  |||||

RESULT 6
Q92IY4 PRELIMINARY; PRT; 589 AA.
AC Q92IY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
DE ABCT3 OR RC0286.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
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OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008594; AAL02824.1; -.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_TRANSPORTER; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 589 AA; 67062 MW; 568DDCAC02B62773 CRC64;

  Query Match          100.0%; Score 31; DB 16; Length 589;
  Best Local Similarity 100.0%; Pred. No. 37;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 511 ATSSLDS 517
  |||||

RESULT 7
Q9L7X7 PRELIMINARY; PRT; 596 AA.
ID Q9L7X7
AC Q9L7X7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC transporter protein (Fragment).
GN EXSA.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL9;
RA Freitas D.A., Miyoshi A., Oliveira S.C., Azevedo V.;
RT "Cloning and sequence analysis of the exsA gene encoding an ABC
RT transporter protein from Brucella abortus.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218367; AAF64672.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
KW ATP-binding.
FT NON_TER 1
SQ SEQUENCE 596 AA; 65461 MW; 3CD7B48078C419C3 CRC64;

  Query Match          100.0%; Score 31; DB 2; Length 596;
  Best Local Similarity 100.0%; Pred. No. 37;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 510 ATSSLDS 516
  |||||

RESULT 8
Q8U6S8 PRELIMINARY; PRT; 600 AA.
ID Q8U6S8
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AC Q8U6S8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC transporter, nucleotide binding/ATPase protein.
GN EXSA OR ATU4728 OR AGR_L309.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorllo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009401; AAL45522.1; -.
DR EMBL; AE008213; AAK88722.1; -.
KW Complete proteome.
SQ SEQUENCE 600 AA; 65880 MW; B74D36107BD753E9 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 600;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 517 ATSSLDS 523

RESULT 9
Q98LY9
ID Q98LY9 PRELIMINARY; PRT; 601 AA.
AC Q98LY9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ATP-binding protein of ABC transporter.
GN MLI0815.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002995; BAB48324.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 601 AA; 65926 MW; 21FE62D90E6D585A CRC64;

Query Match 100.0%; Score 31; DB 16; Length 601;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 518 ATSSLDS 524

RESULT 10
Q52924
ID Q52924 PRELIMINARY; PRT; 604 AA.
AC Q52924;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE EXSA protein (MSBA-like SACCHARIDE EXPORTING ABC transporter protein,
DE CONSISTING of ATP-binding and permease domains).
GN EXSA OR RB1064 OR SMB20941.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / SU47;
RX MEDLINE=96133689; PubMed=8544814;
RA Becker A., Kuester H., Niehaus K., Puehler A.;
RT "Extension of the Rhizobium meliloti succinoglycan biosynthesis gene
RT cluster: identification of the exsA gene encoding an ABC transporter
RT protein, and the exsB gene which probably codes for a regulator of
RT succinoglycan biosynthesis.";
RL Mol. Gen. Genet. 249:487-497(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / SU47;
RA Becker A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBDJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / SU47;
RA York G.M., Walker G.C.;
RL Mol. Microbiol. 25:117-134(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=1021; PLASMID=PSYMB (MEGAPLASMID 2);
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
CC -!- SIMILARITY: BELONGS TO THE ABC_TRANSPORTER FAMILY.
DR EMBL; Z50189; CAA90568.1; -.
DR EMBL; AJ225561; CAA12529.1; -.

DR EMBL; AL603645; CAC49464.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Plasmid; Complete proteome.
SQ SEQUENCE 604 AA; 66094 MW; 2C759C1FF0BAB12A CRC64;

Query Match 100.0%; Score 31; DB 16; Length 604;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 518 ATSSLDS 524
|||||

RESULT 11
Q9W0C5 PRELIMINARY; PRT; 606 AA.
AC Q9W0C5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG7955 protein (GH20617P).
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AE003472; AAF47525.1; -.
DR EMBL; AY051556; AAK92980.1; -.
DR FlyBase; FBgn0035244; CG7955.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 606 AA; 66104 MW; 76C80500A1B62327 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 606;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 511 ATSSLDS 517
|||||

RESULT 12
Q98AT0 PRELIMINARY; PRT; 631 AA.
AC Q98AT0;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ABC transporter, ATP-binding protein, ExsA.
GN MLR5867.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003007; BAB52242.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 631 AA; 69489 MW; A7DAEB1F457A6985 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 631;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLS 7
Db 543 ATSSSLS 549

RESULT 13

Q08667 Q08667 PRELIMINARY; PRT; 947 AA.
AC Q08667;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE transport protein.
GN MDR2.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB3/W2;
RX MEDLINE=94158979; PubMed=8114829;
RA Zalis M.G., Wilson C.M., Zhang Y., Wirth D.F.;
RT "Characterization of the pfmdr2 gene for Plasmodium falciparum
[published erratum appears in Mol Biochem Parasitol 1994
Feb;63(2):311].";
RL Mol. Biochem. Parasitol. 62:83-92(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HB3/W2;
RX MEDLINE=94277156; PubMed=7911976;
RA Zalis M.G., Wilson C.M., Zhang Y., Wirth D.F.;
RT "Characterization of the pfmdr2 gene for Plasmodium falciparum."
RL Mol. Biochem. Parasitol. 63:311-311(1994).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; L13381; AAA61983.1; -.
DR HSSP; P13569; 1NBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 947 AA; 110246 MW; 5D7B1D39515C4C71 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 947;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLS 7
Db 849 ATSSSLS 855

RESULT 14

Q25693 Q25693 PRELIMINARY; PRT; 1025 AA.
AC Q25693;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE pfmdr2 protein.
GN PFMDR2.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D10;
RX MEDLINE=94333528; PubMed=7914495;
RA Rubio J.P., Cowman A.F.;
RT "Plasmodium falciparum: the pfmdr2 protein is not overexpressed in
RT chloroquine-resistant isolates of the malaria parasite.";
RL Exp. Parasitol. 79:137-147(1994).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; U04640; AAA21513.1; -.
DR HSSP; P13569; 1NBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 1025 AA; 119152 MW; 91AF3BD8916D520D CRC64;

Query Match 100.0%; Score 31; DB 5; Length 1025;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels; 0; Gaps 0;

QY 1 ATSSSLS 7
Db 851 ATSSSLS 857

RESULT 15

Q9NG76 Q9NG76 PRELIMINARY; PRT; 1415 AA.
AC Q9NG76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Multidrug resistance protein Pgh1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCCL/HN;
RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RT "Mutations in the multidrug resistance (MDR) gene of Plasmodium
RT falciparum isolate FCC1/HN.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF258325; AAF71750.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtranprtTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transportr; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
KW ATP-binding; Transport.
SQ SEQUENCE 1415 AA; 161797 MW; 8C63811117940427 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 1415;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLS 7
Db 1334 ATSSSLS 1340

Search completed: March 10, 2003, 17:00:08
Job time : 17.4483 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: March 10, 2003, 16:46:26 ; Search time 19.8621 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	127	11	Q925S9 mus musculu
2	40	85.1	312	2	Q57172 acinetobact
3	38	80.9	105	3	Q9Y8E0 pneumocysti
4	38	80.9	475	10	Q9LKB7 arabadopsi
5	35	74.5	476	17	Q8TSH3 methanosarc
6	35	74.5	520	3	P87105 pneumocysti
7	35	74.5	536	17	Q97YP2 sulfolobus
8	35	74.5	547	16	Q988I9 rhizobium l
9	35	74.5	559	16	Q92ND1 rhizobium m
10	35	74.5	619	16	Q8UGT5 agrobacteri
11	35	74.5	671	3	O94113 pneumocysti
12	35	74.5	761	5	Q9TYU3 caenorhabdi
13	35	74.5	784	11	Q925M5 mus musculu
14	35	74.5	784	11	Q91XZ6 mus musculu
15	35	74.5	787	3	O94096 pneumocysti
16	35	74.5	790	3	O13304 pneumocysti

17	35	74.5	874	3	Q96VJ2 pneumocysti
18	35	74.5	897	3	Q96VJ1 pneumocysti
19	35	74.5	926	3	O13305 pneumocysti
20	35	74.5	938	3	Q96VI4 pneumocysti
21	35	74.5	1646	5	Q9VD85 drosophila
22	35	74.5	1887	11	Q9QW67 rattus sp.
23	35	74.5	1898	11	Q9EQ17 mus musculu
24	35	74.5	1898	11	Q64604 r protein-t
25	34	72.3	131	12	Q89240 wheat dwarf
26	34	72.3	211	10	Q9M279 arabadopsi
27	34	72.3	461	16	Q8ZR07 salmonella
28	34	72.3	461	16	Q8Z8I5 salmonella
29	34	72.3	572	4	Q9UG31 homo sapien
30	34	72.3	645	4	O95928 homo sapien
31	34	72.3	721	2	Q9L9L3 pasteurella
32	34	72.3	1254	4	Q96AY4 homo sapien
33	34	72.3	1263	4	Q9UPV8 homo sapien
34	33	70.2	153	12	Q65346 autographa
35	33	70.2	161	10	Q9LUY0 arabadopsi
36	33	70.2	223	17	Q97WP2 sulfolobus
37	33	70.2	230	17	Q9Y979 aeropyrum p
38	33	70.2	283	3	O42871 schizosacch
39	33	70.2	312	2	Q9L796 porphyromon
40	33	70.2	351	16	Q8ZED2 yersinia pe
41	33	70.2	723	11	Q925L6 mus musculu
42	33	70.2	786	11	Q91Y04 mus musculu
43	33	70.2	792	11	Q925L3 mus musculu
44	33	70.2	792	11	Q91Y02 mus musculu
45	33	70.2	802	11	Q91Y03 mus musculu

ALIGNMENTS

RESULT 1					
Q925S9	ID	Q925S9	PRELIMINARY;	PRT;	127 AA.
AC	Q925S9;				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			
DE	Immunoglobulin light chain (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;				
RX	MEDLINE=99306687; Pubmed=10380019;				
RA	Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,				
RA	Foon K.A., Chatterjee S.K.;				
RT	"Construction and characterization of a chimeric fusion protein				
RT	consisting of an anti-idiotypic antibody mimicking a breast cancer-				
RT	associated antigen and the cytokine GM-CSF.";				
RRL	Hybridoma 18:193-202(1999).				
DR	EMBL; AF124721; AAK55120.1; -.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; ig; 1.				
FT	NON_TER 127 127				
SQ	SEQUENCE 127 AA; 13794 MW; 13F61BEBBB981FA5 CRC64;				
Query Match 100.0%; Score 47; DB 11; Length 127;					
Best Local Similarity 100.0%; Pred. No. 0.081;					
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 LQYASSPYT 9				
Db	109 LQYASSPYT 117				
RESULT 2					
Q57172					
;					

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ID AC Q57172 PRELIMINARY; PRT; 312 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Homology to HYDROLASES.
GN ESTB.
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=95400495; PubMed=7670642;
RA Geissdoerfer W.; Frosch C.S.; Haspel G.; Ehrt S.; Hillen W.;
RT "Two genes encoding proteins with similarities to rubredoxin and
RT rubredoxin reductase are required for conversion of dodecane to lauric
RT acid in Acinetobacter calcoaceticus ADP1.";
RL Microbiology 141:1425-1432(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RA Geissdoerfer W.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RA Geissdoerfer W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BD413;
RA Kok R.G.; Bart A.; Hellingwerf K.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z46863; CAA86927.1; -.
DR EMBL; X88895; CAA61351.1; -.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
KW Hydrolase.
SQ SEQUENCE 312 AA; 34680 MW; 14E020BA7654D905 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 312;
Best Local Similarity 77.8%; Pred. No. 5.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db ||::|||||
5 LQFSSSPYT 13

RESULT 3
Q9Y8E0
ID Q9Y8E0 PRELIMINARY; PRT; 105 AA.
AC Q9Y8E0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Subtilisin-like serine protease (Fragment).
GN PRT1.
OS Pneumocystis carinii f. sp. ratti.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=38082;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97388577; PubMed=9245811;
RA Lugli E.B.; Allen A.G.; Wakefield A.E.;
RT "A Pneumocystis carinii multi-gene family with homology to subtilisin-
RT like serine proteases.";
RL Microbiology 143:2223-2236(1997).
RN [2]
```

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RP SEQUENCE FROM N.A.
RA Lugli E.B.; Bampton E.T.; Ferguson D.J.P.; Wakefield A.E.;
RT "Cell Surface protease PRT1 identified in the fungal pathogen
RT Pneumocystis carinii.";
RL Mol. Microbiol. 31:0-0(1999).
DR EMBL; AF126252; AAD39924.1; -.
DR MEROPS; S08.011; -.
DR InterPro; IPR000209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.
KW Protease.
FT NON_TER 1 1
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11163 MW; 8C00CE05BE61BAAB CRC64;

Query Match 80.9%; Score 38; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
Db |||||||
51 YASSPYT 57

RESULT 4
Q9LKB7
ID Q9LKB7 PRELIMINARY; PRT; 475 AA.
AC Q9LKB7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gb|AAB82637.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T.; Kato T.; Sato S.; Nakamura Y.; Asamizu E.; Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000370; BAA97050.1; -.
SQ SEQUENCE 475 AA; 54738 MW; 39DAE2288B590701 CRC64;

Query Match 80.9%; Score 38; DB 10; Length 475;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYASSPY 8
Db |||||
106 LQYQSPY 113

RESULT 5
Q8TSH3
ID Q8TSH3 PRELIMINARY; PRT; 476 AA.
AC Q8TSH3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ss-DNA-specific exonuclease.
GN RECJ OR MA0823.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
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Db      172 YANSPYT 178
|||||
RESULT 7
Q97YP2      PRELIMINARY;      PRT;      536 AA.
AC      Q97YP2
DT      01-OCT-2001 (TrEMBLrel. 18, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Oligo/dipeptide transport, permease protein (dppC-2).
GN      DPPC-2 OR SS01283.
OS      Sulfolobus solfataricus.
OC      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC      Sulfolobus.
OX      NCBI_TaxID=2287;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 35092 / DSM 1617 / P2;
RX      MEDLINE=21332296; PubMed=11427726;
RA      She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA      Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA      De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA      Heikamp-de Jong I., Jeffries A.C., Kozer A.C.J., Medina N., Peng X.,
RA      Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA      Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA      Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT      "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RRL      proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR      EMBL; AE006742; AAK41520.1; -.
DR      InterPro; IPR000515; BPD_transp.
DR      Pfam; PF00528; BPD_transp; 1.
DR      PROSITE; PS00402; BPD_TRANSF_INN_MEMBR; 1.
KW      Complete proteome.
SQ      SEQUENCE 536 AA; 59322 MW; 134A43BD8C60D3EF CRC64;

Query Match      74.5%; Score 35; DB 17; Length 536;
Best Local Similarity 85.7%; Pred.No. 92;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps

QY      2 QYASSPY 8
|||||
Db      47 QYAASPY 53
|||||

RESULT 8
Q988I9      PRELIMINARY;      PRT;      547 AA.
AC      Q988I9;
DT      01-OCT-2001 (TrEMBLrel. 18, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Hypothetical protein mll6723.
GN      MLL6723.
OS      Rhizobium loti (Mesorhizobium loti).
OC      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC      Phyllobacteriaceae; Mesorhizobium.
OX      NCBI_TaxID=381;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MAFF303099;
RX      MEDLINE=21082930; PubMed=11214968;
RA      Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA      Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA      Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA      Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA      Takeuchi C., Yamada M., Tabata S.;
RT      "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT      Mesorhizobium loti.";
RRL      DNA Res. 7:331-338(2000).
DR      EMBL; AP003010; BAB52961.1; -.
KW      Hypothetical protein; Complete proteome.

```

SQ SEQUENCE 547 AA; 60809 MW; 89BBF8D4D2B88499 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 547;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
||||| |

Db 450 LQYASDPVT 458

RESULT 9

Q92ND1 ID Q92ND1 PRELIMINARY; PRT; 559 AA.

AC Q92ND1;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical transmembrane protein SMC01665.

GN R02277 OR SMC01665.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Sinorhizobium.

OX NCBI_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1021;

RX MEDLINE=21396507; PubMed=11481430;

RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

DR EMBL; AL591790; CAC46856.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 559 AA; 61358 MW; 1663C17276640F4F CRC64;

Query Match 74.5%; Score 35; DB 16; Length 559;
Best Local Similarity 77.8%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
||||| |

Db 463 LQYASDPVT 471

RESULT 10

Q8UGT5 ID Q8UGT5 PRELIMINARY; PRT; 619 AA.

AC Q8UGT5;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Hypothetical protein Atu0950.

GN ATU0950 OR AGR_C_1734.

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=176299;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21608550; PubMed=11743193;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Glendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";

RL Science 294:2317-2323(2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21608551; PubMed=11743194;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurolo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;

RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";

RL Science 294:2323-2328(2001).

DR EMBL; AE009059; AAL41964.1; -.

DR EMBL; AE008025; AAK86755.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 619 AA; 68652 MW; EE66684BCB04A2C9 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 619;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
||||| |

Db 517 LQYASDPIT 525

RESULT 11

O94113 ID O94113 PRELIMINARY; PRT; 671 AA.

AC O94113;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Kexin (Fragment).

GN KEXIN.

OS Pneumocystis carinii.

OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;

OC Pneumocystis.

OX NCBI_TaxID=4754;

RN [1]

RP SEQUENCE FROM N.A.

RA Russian D.A., Andrawis-Sorial V., Angus C.W., Kovacs J.A.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U82999; AAD00541.1; -.

DR MEROPS; S08.011; -.

DR InterPro; IPR000209; Peptidase_S8.

DR InterPro; IPR002884; P_domain.

DR InterPro; IPR002965; P_rich_extensn.

DR Pfam; PF01483; P; 1.

DR Pfam; PF00082; Peptidase_S8; 1.

DR PRINTS; PR01217; PRICHEXTENS.

DR PRINTS; PR00723; SUBTILISIN.

DR ProDom; PD000717; P_domain; 1.

DR PROSITE; PS00137; SUBTILASE_HIS; 1.

DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 671 AA; 74049 MW; BAC4A164EC007C2E CRC64;

Query Match 74.5%; Score 35; DB 3; Length 671;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
||:||||

Db 177 YANSPYT 183

RESULT 12

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Q9TYU3
ID Q9TYU3 PRELIMINARY; PRT; 761 AA.
AC Q9TYU3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 88.4 kDa protein.
GN VC5.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Tin-Wollam A.M., Wohldmann P.;
RT "The sequence of C. elegans cosmid VC5.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AF106581; AAC78212.1; -.
DR HSSP; P20393; 1A6Y.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 2.
DR Pfam; PF00105; zf-C4; 2.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 2.
DR SMART; SM00430; HOLI; 2.
DR SMART; SM00399; Znf_C4; 2.
KW DNA-binding; Hypothetical protein; Nuclear protein; Receptor;
KW Transcription regulation; Zinc-finger.
SQ SEQUENCE 761 AA; 88417 MW; FFD60271DF28ED2D CRC64;

Query Match 74.5%; Score 35; DB 5; Length 761;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
I:|||||
Db 99 YSSSPYT 105

RESULT 13
Q925M5
ID Q925M5 PRELIMINARY; PRT; 784 AA.
AC Q925M5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Protocadherin-betaD.
GN PCDHB4 OR PCDHB5A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21223055; PubMed=11322959;
```

```
RA Vanhalst K., Kools P., Vanden Eynde E., van Roy F.;
RT "The human and murine protocadherin-beta one-exon gene families show
high evolutionary conservation, despite the difference in gene
number.";
RL FEBS Lett. 495:120-125(2001).
CC -!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
DR EMBL; AF326297; AAK53222.1; -.
DR MGD; MGI:2136738; Pcdhb4.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; cadherin; 5.
DR PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
DR PROSITE; PS50268; CADHERIN_2; 6.
KW Calcium-binding; Cell adhesion; Glycoprotein.
SQ SEQUENCE 784 AA; 85819 MW; 9C0524BCF3A81F45 CRC64;

Query Match 74.5%; Score 35; DB 11; Length 784;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
I:|||||
Db 564 LQNASAPYT 572

RESULT 14
Q91XZ6
ID Q91XZ6 PRELIMINARY; PRT; 784 AA.
AC Q91XZ6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Protocadherin beta 4.
GN PCDHB4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99308636; PubMed=10380929;
RA Wu Q., Maniatis T.;
RT "A striking organization of a large family of human neural cadherin-
like cell adhesion genes.";
RL Cell 97:779-790(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20202599; PubMed=10716726;
RA Wu Q., Maniatis T.;
RT "Large exons encoding multiple ectodomains are a characteristic
feature of protocadherin genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21154914; PubMed=11230163;
RA Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz J.,
RA Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T.;
RT "Comparative dna sequence analysis of mouse and human protocadherin
gene clusters.";
RL Genome Res. 11:389-404(2001).
CC -!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
DR EMBL; AY013786; AAK26075.1; -.
DR MGD; MGI:2136738; Pcdhb4.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; cadherin; 5.
DR PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
DR PROSITE; PS50268; CADHERIN_2; 6.
KW Calcium-binding; Cell adhesion; Glycoprotein.
SQ SEQUENCE 784 AA; 85778 MW; 13A0337BBAAE26FC CRC64;

Query Match 74.5%; Score 35; DB 11; Length 784;
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Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
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Db 564 LQNASAPYT 572

RESULT 15
O94096
ID O94096 PRELIMINARY; PRT; 787 AA.
AC O94096;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Kexin.
GN KEX.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RA Russian D.A., Edman J.C., Angus C.W., Sorial V., Turner R.,
RA Kovacs J.A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U62910; AAD00101.1; -.
DR HSSP; P00782; 2SBT.
DR MEROPS; S08.011; -.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR InterPro; IPR002965; P_rich_extensn.
DR Pfam; PF01483; P; 1.
DR PRINTS; PF00082; Peptidase_S8; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
SQ SEQUENCE 787 AA; 88916 MW; 2C9F572BF636632F CRC64;

Query Match 74.5%; Score 35; DB 3; Length 787;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
|||
Db 362 YANSPYT 368

Search completed: March 10, 2003, 17:00:10
Job time : 21.8621 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 6.82759 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	42	77.8	130	1	KV5G_MOUSE	P01639 mus musculu
2	37	68.5	234	1	YP52_YEAST	P36018 saccharomyc
3	37	68.5	527	1	MET3_CANAL	Q9y872 candida alb
4	34	63.0	251	1	RS3A_SCHPO	Q09781 schizosacch
5	34	63.0	494	1	ICSB_SHIFL	P33546 shigella fl
6	34	63.0	650	1	DNAK_BURPS	O68191 burkholderi
7	34	63.0	876	1	SYV_MYCTU	O53175 mycobacteri
8	34	63.0	920	1	CO4_BOVIN	P01030 bos taurus
9	33	61.1	115	1	KV5I_MOUSE	P01642 mus musculu
10	33	61.1	237	1	YM9A_YEAST	Q04902 saccharomyc
11	33	61.1	322	1	CGM2_SCHPO	P36613 schizosacch
12	33	61.1	415	1	CSCB_ECOLI	P30000 escherichia
13	33	61.1	529	1	KPYK_CHICK	P00548 gallus gall
14	33	61.1	641	1	DNAK_METSS	Q9zfc6 methylovoru
15	33	61.1	656	1	DNAK_ALCEU	O33522 alcaligenes
16	33	61.1	663	1	MNEL_YEAST	P24720 saccharomyc
17	32	59.3	103	1	CHLB_SELMO	P37856 selaginella
18	32	59.3	162	1	CBP6_YEAST	P07253 saccharomyc
19	32	59.3	183	1	YH96_ARCFU	O28478 archaeoglob
20	32	59.3	261	1	RS3A_ORYSA	P49397 oryza sativ
21	32	59.3	335	1	GCP_AQUAE	O66986 aquifex aeo
22	32	59.3	388	1	SUCC_SALTY	Q8xep0 salmonella
23	32	59.3	403	1	YNR5_YEAST	P53883 saccharomyc
24	32	59.3	404	1	TRPB_METJA	Q60179 methanococc
25	32	59.3	512	1	GUAA_CHLMU	Q9pkm3 chlamydia m
26	32	59.3	530	1	KPY1_RABIT	P11974 oryctolagus
27	32	59.3	530	1	KPY2_RABIT	O18919 oryctolagus
28	32	59.3	650	1	DNAK_BURCE	P42373 burkholderi
29	32	59.3	715	1	GREA_CHLTR	O84641 chlamydia t
30	32	59.3	1229	1	KPBA_DROME	Q9w391 drosophila
31	31	57.4	108	1	KV5K_MOUSE	P01644 mus musculu
32	31	57.4	108	1	KV5L_MOUSE	P01645 mus musculu
33	31	57.4	108	1	KV5M_MOUSE	P01646 mus musculu

RESULT 1				
KV5G_MOUSE				
ID	KV5G_MOUSE	STANDARD;	PRT;	130 AA.
AC	P01639; P01640;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-V region MOPC 41 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=79221900; PubMed=111146;			
RA	Seidman J.G., Max E.E., Leder P.;			
RT	"A kappa-immunoglobulin gene is formed by site-specific recombination			
RT	without further somatic mutation.";			
RL	Nature 280:370-375(1979).			
RN	[2]			
RP	SEQUENCE OF 1-33.			
RX	MEDLINE=77148916; PubMed=403522;			
RA	Burstein Y., Schechter I.;			
RT	"Amino acid sequence of the NH2-terminal extra piece segments of the			
RT	precursors of mouse immunoglobulin lambda1-type and kappa-type light			
RT	chains.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).			
RN	[3]			
RP	SEQUENCE OF 23-130.			
RX	MEDLINE=67056897; PubMed=4162931;			
RA	Gray W.R., Dreyer W.J., Hood L.;			
RT	"Mechanism of antibody synthesis: size differences between mouse			
RT	kappa chains.";			
RL	Science 155:465-467(1967).			
CC	-!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE			
CC	SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.			
CC	-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A01922; KVM5M4.			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region; Signal; Bence-Jones protein.			
FT	SIGNAL 1 22			
FT	CHAIN 23 130			
FT	DOMAIN 23 45			
FT	DOMAIN 46 56			
FT	DOMAIN 57 71			
FT	DOMAIN 72 78			
FT	DOMAIN 79 110			
FT	DOMAIN 111 119			
FT	DOMAIN 120 129			
FT	DISULFID 45 110			
FT	VARIANT 1 2			
FT	NON TER 130			

ALIGNMENTS

34	31	57.4	108	1	KV5N_MOUSE	P01647 mus musculu
35	31	57.4	108	1	KV5O_MOUSE	P01648 mus musculu
36	31	57.4	108	1	KV5P_MOUSE	P01649 mus musculu
37	31	57.4	115	1	KV5F_MOUSE	P01638 mus musculu
38	31	57.4	128	1	KV5E_MOUSE	P01637 mus musculu
39	31	57.4	169	1	SNFB_YEAST	P38956 saccharomyc
40	31	57.4	188	1	Y101_UREPA	Q9pr43 ureaplasma
41	31	57.4	251	1	RS3B_SCHPO	O94438 schizosacch
42	31	57.4	275	1	YMA9_CAEEL	P34454 caenorhabdi
43	31	57.4	293	1	YNEJ_ECOLI	P77309 escherichia
44	31	57.4	385	1	GBA1_SOYBN	P49084 glycine max
45	31	57.4	399	1	Y538_STRPY	Q9a0z8 streptococc


```
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=2184801; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [2]
RP SEQUENCE OF 1-71 FROM N.A.
RC STRAIN=968 h90;
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hiraoka Y.;
RT "Large-scale screening of intracellular protein localization in living
RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
CC -!- MISCELLANEOUS: THERE ARE TWO GENES FOR S1 IN S.POMBE.
CC -!- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL; Z54308; CAA91095.1; -.
CC EMBL; AB027994; BAA87298.1; -.
CC InterPro; IPR001593; Ribosomal_S3AE.
CC Pfam; PF01015; Ribosomal_S3AE; 1.
CC ProDom; PD003035; Ribosomal_S3AE; 1.
CC PROSITE; PS01191; RIBOSOMAL_S3AE; 1.
KW Ribosomal protein; Multigene family.
FT INIT_MET 0 BY SIMILARITY.
SQ SEQUENCE 251 AA; 28357 MW; 2A254B63415A9B98 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 251;
Best Local Similarity 75.0%; Pred. NO. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
Db 234 SQDVGSKV 241

RESULT 5
ICSB_SHIFL
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ID ICSB_SHIFL STANDARD; PRT; 494 AA.
AC P33546;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Intercellular spread protein.
GN ICSB.
OS Shigella flexneri.
OG Plasmid 210 kb invasion pWR100.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / Serotype 5;
RX MEDLINE=92356824; PubMed=1495389;
RA Allaoui A., Mounier J., Prevost M.-C., Sansonetti P.J., Parsot C.;
RT "icsB: a Shigella flexneri virulence gene necessary for the lysis of
RT protrusions during intercellular spread.";
RL Mol. Microbiol. 6:1605-1616(1992).
RN [2]
RP SEQUENCE OF 1-19 FROM N.A.
RC STRAIN=M90T / Serotype 5;
RX MEDLINE=93239268; PubMed=8478058;
RA Allaoui A., Menard R., Sansonetti P.J., Parsot C.;
RT "Characterization of the Shigella flexneri ipgD and ipgF genes, which
RT are located in the proximal part of the mxi locus.";
RL Infect. Immun. 61:1707-1714(1993).
CC -!- FUNCTION: NECESSARY FOR THE LYSIS OF PROTRUSIONS DURING
CC INTERCELLULAR SPREAD.
CC -!- SUBCELLULAR LOCATION: PERIPLASMIC. THE PERIPLASM MAY REPRESENT
CC A RESERVOIR FOR THE PROTEIN, IT WOULD BE RELEASED AT A LATER
CC STAGE DURING THE INFECTION CYCLE.
CC -----
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CC -----
CC EMBL; M86530; AAD15221.1; -.
CC PIR; S22687; S22687.
KW Plasmid; Virulence; Periplasmic.
SQ SEQUENCE 494 AA; 56323 MW; DC975ECB76FB57BB CRC64;

Query Match 63.0%; Score 34; DB 1; Length 494;
Best Local Similarity 66.7%; Pred. NO. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDIGSKLY 11
Db 467 SPDLGTKLY 475

RESULT 6
DNAK_BURPS
ID DNAK_BURPS STANDARD; PRT; 650 AA.
AC O68191;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
GN DNAK.
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=28450;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23343;
```

RA See L.H., Yap E.H., Yap E.P.H.;
RT "Isolation and sequencing of the heat shock protein 70 (hsp70/dnaK)
RT gene in Burkholderia pseudomallei.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; AF016711; AAC15473.1; -.
DR HSSP; P04475; 1DG4.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 200 200 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 650 AA; 69735 MW; BE46330B6DE174D0 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 650;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
|||:| |:
Db 597 ASQKLGEKMY 606

RESULT 7
SYV_MYCTU STANDARD; PRT; 876 AA.
ID SYV_MYCTU STANDARD; PRT; 876 AA.
AC O53175;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
GN VALS OR RV2448C OR MT2524 OR MTV008.04C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AL021246; CAA16025.1; -.
DR EMBL; AE007089; AAK46823.1; -.
DR HSSP; P96142; 1GAX.
DR TIGR; MT2524; -.
DR Tuberculist; RV2448C; -.
DR InterPro; IPR002300; tRNA-synt_la.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002303; tRNA-synt_val.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHVAL.
DR TIGRFAMS; TIGR00422; vals; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 43 53 "HIGH" REGION.
FT SITE 530 534 "KMSKS" REGION.
FT BINDING 533 533 ATP (BY SIMILARITY).
SQ SEQUENCE 876 AA; 97820 MW; 85C4E2C3BF76B090 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 876;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
|||:| |:
Db 575 RASRNFGTKLF 585

RESULT 8
CO4_BOVIN STANDARD; PRT; 920 AA.
ID CO4_BOVIN STANDARD; PRT; 920 AA.
AC P01030; Q27993; Q27992;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C4 precursor [Contains: C4A anaphylatoxin] (Fragments).
GN C4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-77.
RX MEDLINE=83126436; PubMed=6760852;
RA Smith M.A., Gerrie L.M., Dunbar B., Fothergill J.E.;
RT "Primary structure of bovine complement activation fragment C4a, the
RT third anaphylatoxin. Purification and complete amino acid sequence.";
RL Biochem. J. 207:253-260(1982).
RN [2]
RP SEQUENCE OF 78-920 FROM N.A.
RC TISSUE=Liver;
RA Groth D.M.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE

CC CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY
CC ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
CC ANAPHYLATOXIN.
CC -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4,
CC C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES.
CC -!- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR
CC AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
CC OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
CC -!- MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
CC PROTEIN.
CC -!- SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.
CC -!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; U16750; AAA52751.1; -.
DR EMBL; U16749; AAA52750.1; -.
DR PIR; A01265; C4BOAT.
DR HSSP; P01031; 1CFA.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxn.
DR InterPro; IPR001599; MacrogloblnA2.
DR InterPro; IPR001134; Netrin_C.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2-MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Plasma; Glycoprotein; Sulfation;
KW Inflammatory response.
FT NON_TER 1 1
FT NON_CONS 77 78
FT NON_CONS 342 343
FT CHAIN 1 622
FT PROPEP 623 629
FT CHAIN 630 920
FT PEPTIDE 1 77
FT DOMAIN 23 57
FT DISULFID 23 49
FT DISULFID 24 56
FT DISULFID 37 57
FT THIOLEST 191 194
FT MOD_RES 593 593
FT MOD_RES 596 596
FT MOD_RES 598 598
FT CARBOHYD 504 504
FT CARBOHYD 567 567
SQ SEQUENCE 920 AA; 101881 MW; 1425A0BD945F5497 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 920;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDIGSKLY 11
Db 397 AKDIGDKLY 405

RESULT 9
KV5I_MOUSE
ID KV5I_MOUSE STANDARD; PRT; 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81220975; PubMed=6264318;
RA Pech M., Hocht J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
CC PIR; A01925; KVMSL7.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 115;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
Db 44 RASQSIGTSIH 54

RESULT 10
YM9A_YEAST
ID YM9A_YEAST STANDARD; PRT; 237 AA.
AC Q04902;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 26.0 kDa protein in FET4-ERR1 intergenic region.
GN YMR322C OR YM9924.14C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE YMR322C/YOR391C/YPL280W (YEAST),
CC SPAC1F7.06/SPAC5H10.02C/SPAC1D3.13 (S.POMBE FAMILY).
CC -----
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CC -----

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CC -----
DR EMBL; Z54141; CAA90840.1; -.
DR SGD; S0004941; YMR322C.
DR InterPro; IPR002818; ThiJ.
DR Pfam; PF01965; ThiJ; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 26039 MW; 004EA3E702332905 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 237;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QDIGSKLY 11
Db 121 QDIASKIY 128

RESULT 11
CGM2_SCHPO
ID CGM2_SCHPO STANDARD; PRT; 322 AA.
AC P36613;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cyclin mcs2 (Mitotic catastrophe suppressor 2).
GN MCS2 OR SPBP16F5.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=93223713; PubMed=8467814;
RA Molz L., Beach D.;
RT "Characterization of the fission yeast mcs2 cyclin and its associated
RT protein kinase activity.";
RL EMBO J. 12:1723-1732(1993).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: ESSENTIAL FOR PROGRESSION THROUGH THE CELL CYCLE.
CC -!- PROBABLY INTERACTS WITH A PROTEIN KINASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
CC -----
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CC -----
DR EMBL; S59895; AAB26193.1; -.
DR EMBL; AL441603; CAC08541.1; -.
DR PIR; S35380; S35380.
DR HSSP; P51946; IKXU.
DR InterPro; IPR005258; Ccl1.
DR InterPro; IPR004366; Cyclin.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR TIGRFAMS; TIGR00569; ccl1; 1.
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
KW Cyclin; Cell cycle; Cell division; Nuclear protein.
SQ SEQUENCE 322 AA; 37673 MW; 09B8DDDB46563727C CRC64;

Query Match 61.1%; Score 33; DB 1; Length 322;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
Db 266 KKAQDYGRKLY 276

RESULT 12
CSCB_ECOLI
ID CSCB_ECOLI STANDARD; PRT; 415 AA.
AC P30000;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sucrose transport protein (sucrose permease).
GN CSCB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=EC3132;
RX MEDLINE=93062804; PubMed=1435727;
RA Bockmann J., Heuel H., Lengeler J.W.;
RT "Characterization of a chromosomally encoded, non-PTS metabolic
RT pathway for sucrose utilization in Escherichia coli EC3132.";
RL Mol. Gen. Genet. 235:22-32(1992).
CC -!- FUNCTION: PROTON SYMPORT TRANSPORT SYSTEM. HAS AN ESSENTIAL
CC ROLE IN SUCROSE METABOLISM.
CC -!- PATHWAY: Sucrose metabolism.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: BELONGS TO THE LACY/RAFB FAMILY OF PERMEASES.
CC -----
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CC -----
DR EMBL; X63740; CAA45274.1; -.
DR EMBL; X81461; CAA57217.1; -.
DR PIR; S19880; GRECST.
DR InterPro; IPR000576; Lacy_symp.
DR Pfam; PF01306; Lacy_symp; 1.
DR PRINTS; PR00174; LACYSMPORT.
DR TIGRFAMS; TIGR00882; 2A0105; 1.
DR PROSITE; PS00896; LACY_1; 1.
CC -----
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DR PROSITE; PS00897; LACY_2; 1.
KW Transport; Sugar transport; Symport; Inner membrane; Transmembrane.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 48
FT TRANSMEM 49 69
FT DOMAIN 70 77
FT TRANSMEM 78 98
FT DOMAIN 99 105
FT TRANSMEM 106 126
FT DOMAIN 127 147
FT TRANSMEM 148 166
FT DOMAIN 167 169
FT TRANSMEM 170 190
FT DOMAIN 191 220
FT TRANSMEM 221 241
FT DOMAIN 242 260
FT TRANSMEM 261 281
FT DOMAIN 282 288
FT TRANSMEM 289 309
FT DOMAIN 310 312
FT TRANSMEM 313 332
FT DOMAIN 333 342
FT TRANSMEM 343 363
FT DOMAIN 364 377
FT TRANSMEM 378 398
FT DOMAIN 399 415
SQ SEQUENCE 415 AA; 46923 MW; D05BBD305B61AC22 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 415;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDIGSKLY 11
I : : : :
Db 251 SHDVGTRLY 259

RESULT 13
KPYK_CHICK
ID KPYK_CHICK STANDARD; PRT; 529 AA.
AC P00548;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pyruvate kinase, muscle isozyme (EC 2.7.1.40).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83221656; PubMed=6574503;
RA Lonberg N., Gilbert W.;
RT "Primary structure of chicken muscle pyruvate kinase mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3661-3665(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099332; PubMed=2981634;
RA Lonberg N., Gilbert W.;
RT "Intron/exon structure of the chicken pyruvate kinase gene.";
RL Cell 40:81-90(1985).
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
CC -!- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.
CC -!- PATHWAY: Glycolysis; final step.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- MISCELLANEOUS: THIS ACTIVITY IS REGULATED BY GLUCOSE LEVELS.
CC -!- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.

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CC EMBL; AF106835; AAC95378.1; -.
DR HSSP; P04475; 1DG4.
DR InterPro; IPR001023; Hsp70.

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DR EMBL; J00903; AAA49021.1; -.
DR EMBL; M18793; AAA49020.1; -.
DR EMBL; M10619; AAA49020.1; JOINED.
DR EMBL; M18788; AAA49020.1; JOINED.
DR EMBL; M18789; AAA49020.1; JOINED.
DR EMBL; M18790; AAA49020.1; JOINED.
DR EMBL; M18791; AAA49020.1; JOINED.
DR EMBL; M18792; AAA49020.1; JOINED.
DR PIR; A00659; KICHPM.
DR HSSP; P11974; 1PKN.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF00224; PK; 1.
DR Pfam; PF02887; PK_C; 1.
DR PRINTS; PR01050; PYRUVTKNASE.
DR ProDom; PD001009; Pyruvate_kinase; 1.
DR TIGRFAMS; TIGR01064; pyruv_kin; 1.
DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
KW Transferase; Kinase; Glycolysis; Phosphorylation; Magnesium.
FT INIT_MET 0
FT ACT_SITE 268 268 BY SIMILARITY.
FT METAL 270 270 MAGNESIUM (POTENTIAL).
FT METAL 291 291 MAGNESIUM (POTENTIAL).
FT METAL 292 292 MAGNESIUM (POTENTIAL).
SQ SEQUENCE 529 AA; 57883 MW; 8B1907B8D31EB72F CRC64;

Query Match 61.1%; Score 33; DB 1; Length 529;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DIGSKLY 11
I : : : :
Db 167 DVGSKIY 173

RESULT 14
DNAK_METSS
ID DNAK_METSS STANDARD; PRT; 641 AA.
AC Q92FC6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
GN DNAK.
OS Methylovorus sp. (strain SS1 / DSM 11726).
OC Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
OC Methylovorus.
OX NCBI_TaxID=81683;
RN [1]
RP SEQUENCE FROM N.A.
RA Eom C.Y., Kim Y.M.;
RT "grpE, dnaK, and dnaJ genes of Methylovorus sp. strain SS1 DSM11726.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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CC EMBL; AF106835; AAC95378.1; -.
DR HSSP; P04475; 1DG4.
DR InterPro; IPR001023; Hsp70.

Job time : 7.82759 secs

DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 199 199 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 641 AA; 69764 MW; 7DFA5EBE144825CB CRC64;

Query Match 61.1%; Score 33; DB 1; Length 641;
Best Local Similarity 60.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
||| :| | :|
Db 594 ASQKLGEKVY 603

RESULT 15
DNAME_ALCEU STANDARD; PRT; 656 AA.
AC O33522;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
GN DNAME.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH34;
RA Talbi S., van der Lelie D.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBDJ databases.
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; AJ001727; CAA04955.1; -.
DR HSSP; P04475; 1DG4.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 200 200 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 656 AA; 71300 MW; 5C7D5D2CE22F5F97 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 656;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
||| :| | :|
Db 595 ASQKLGEKVY 604

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 4.34483 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDs 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	31	100.0	130	1	KV5G_MOUSE	P01639 mus musculu
2	31	100.0	555	1	YNS2_YEAST	P53877 saccharomyc
3	31	100.0	694	1	ABC7_MOUSE	Q61102 mus musculu
4	31	100.0	752	1	ABC7_HUMAN	O75027 homo sapien
5	31	100.0	1419	1	MDR_PLAFF	P13568 plasmodium
6	29	93.5	2404	1	SON_MOUSE	Q9qx47 mus musculu
7	29	93.5	2426	1	SON_HUMAN	P18583 homo sapien
8	28	90.3	584	1	LMRA_LACLA	Q9chl8 lactococcus
9	28	90.3	584	1	LMRA_LACLC	P97046 lactococcus
10	28	90.3	586	1	Y4GM_RHISN	P55469 rhizobium s
11	28	90.3	607	1	HEPA_ANASP	P22638 anabaena sp
12	28	90.3	614	1	YA51_HAEIN	Q57180 haemophilus
13	28	90.3	685	1	MDL1_CANAL	P97998 candida alb
14	28	90.3	695	1	MDL1_YEAST	P33310 saccharomyc
15	28	90.3	698	1	CVAB_ECOLI	P22520 escherichia
16	28	90.3	698	1	MCHF_ECOLI	Q9exn5 escherichia
17	28	90.3	1280	1	MDR1_LEIEN	Q06034 leishmania
18	28	90.3	1362	1	PMD1_SCHPO	P36619 schizosacch
19	28	90.3	1444	1	DPO3_LISIN	Q92c34 listeria in
20	28	90.3	1444	1	DPO3_LISMO	Q8y7g1 listeria mo
21	27	87.1	176	1	SSB_TREPA	O83101 treponema p
22	27	87.1	237	1	LECA_DOLLA	P38662 dolichos la
23	27	87.1	302	1	KLF7_HUMAN	O75840 homo sapien
24	27	87.1	432	1	WDRI_HUMAN	Q9bv38 homo sapien
25	27	87.1	463	1	YHCL_BACSU	P54596 bacillus su
26	27	87.1	709	1	WHIT_ANOAL	Q16928 anopheles a
27	27	87.1	717	1	COMA_STRPN	Q03727 streptococc
28	27	87.1	754	1	TBP6_YEAST	P40328 saccharomyc
29	27	87.1	997	1	T257_ECOLI	P25239 escherichia
30	26	83.9	362	1	SEVE_DICDI	P10733 dictyosteli
31	26	83.9	593	1	MDLB_ECOLI	P75706 escherichia
32	26	83.9	725	1	AGAL_YEAST	P32323 saccharomyc
33	26	83.9	802	1	CIKB_RAT	Q63099 rattus norv

34	26	83.9	806	1	CIKB_CANFA	Q95167 canis famil
35	26	83.9	806	1	CIKB_HUMAN	Q92953 homo sapien
36	25	80.6	137	1	COFI_DICDI	P54706 dictyosteli
37	25	80.6	162	1	PHA2_PSEA9	Q52452 pseudanabae
38	25	80.6	185	1	VCO7_ADE40	Q89532 human adeno
39	25	80.6	311	1	CDX2_MOUSE	P43241 mus musculu
40	25	80.6	313	1	HXAB_HUMAN	P31270 homo sapien
41	25	80.6	313	1	KREL_YEAST	P17260 saccharomyc
42	25	80.6	388	1	KG2B_MARGL	P15206 marthasteri
43	25	80.6	394	1	CG2B_ASTPE	P18063 asterina pe
44	25	80.6	416	1	TR19_MOUSE	Q9j1l3 mus musculu
45	25	80.6	448	1	YO26_MYCTU	P71596 mycobacteri

ALIGNMENTS

RESULT 1
KV5G_MOUSE
ID KV5G_MOUSE STANDARD; PRT; 130 AA.
AC P01639; P01640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 41 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79221900; PubMed=111146;
RA Seidman J.G., Max E.E., Leder P.;
RT "A kappa-immunoglobulin gene is formed by site-specific recombination
without further somatic mutation.";
RL Nature 280:370-375(1979).
RN [2]
RP SEQUENCE OF 1-33.
RX MEDLINE=77148916; PubMed=403522;
RA Burstein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
precursors of mouse immunoglobulin lambda1-type and kappa-type light
chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN [3]
RP SEQUENCE OF 23-130.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.;
RT "Mechanism of antibody synthesis: size differences between mouse
kappa chains.";
RL Science 155:465-467(1967).
CC -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01922; KVM5M4.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal; Bence-Jones protein.
FT SIGNAL 1 22
FT CHAIN 23 130 IG KAPPA CHAIN V-V REGION MOPC 41.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT VARIANT 1 2 MISSING (IN 25% OF THE MOLECULES).
FT NON_TER 130 130

```
SQ SEQUENCE 130 AA; 14311 MW; 5EFE0FE71D5F1BEC CRC64;
Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDs 7
Db 72 ATSSLDs 78

RESULT 2
YNS2_YEAST STANDARD; PRT; 555 AA.
AC P53877;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 61.8 kDa Trp-Asp repeats containing protein in NPR1-RPS3
DE intergenic region.
GN YNL182C OR N1636.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaier B., Piravandi E., Rinke M., Domdey H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: TO S.POMBE SPAC13G7.08C.
CC -----
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CC -----
DR EMBL; Z71458; CAA96075.1; -.
DR SGD; S0005126; YNL182C.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT REPEAT 90 133 WD 1.
FT REPEAT 137 176 WD 2.
FT REPEAT 187 234 WD 3.
FT REPEAT 342 383 WD 4.
SQ SEQUENCE 555 AA; 61773 MW; 8EED6854DF9405A6 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDs 7
Db 506 ATSSLDs 512

RESULT 3
ABC7_MOUSE STANDARD; PRT; 694 AA.
AC Q61102;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family B, member 7, mitochondrial (ATP-
DE binding cassette transporter 7) (ABC transporter 7 protein)
```

```
DE (Fragment).
GN ABCB7 OR ABC7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=97288528; PubMed=9143506;
RA Savary S., Allikmets R., Denizot F., Luciani M.-F., Mattei M.-G.,
RA Dean M., Chimini G.;
RT "Isolation and chromosomal mapping of a novel ATP-binding cassette
RT transporter conserved in mouse and human.";
RL Genomics 41:275-278(1997).
CC -!- FUNCTION: COULD BE INVOLVED IN THE TRANSPORT OF HEME FROM THE
CC MITOCHONDRIA TO THE CYTOSOL. PLAYS A CENTRAL ROLE IN THE
CC MATURATION OF CYTOSOLIC IRON-SULFUR (FE/S) CLUSTER-CONTAINING
CC PROTEINS (By similarity).
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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CC -----
DR EMBL; U43892; AAC53152.1; -.
DR MGD; MGI:109533; Abcb7.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranprtrTM.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transmembrane; Transport; Mitochondrion; Inner membrane.
FT NON_TER 1
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 233 253 POTENTIAL.
FT TRANSMEM 326 346 POTENTIAL.
FT NP_BIND 447 454 ATP (POTENTIAL).
SQ SEQUENCE 694 AA; 76417 MW; A7AE89EAE9AA981D CRC64;

Query Match 100.0%; Score 31; DB 1; Length 694;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDs 7
Db 577 ATSSLDs 583

RESULT 4
ABC7_HUMAN STANDARD; PRT; 752 AA.
AC O75027; O75345; Q9UND1; Q9UP01; Q9BRE1;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family B, member 7, mitochondrial precursor
DE (ATP-binding cassette transporter 7) (ABC transporter 7 protein).
GN ABCB7 OR ABC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98284536; PubMed=9621516;
RA Shimada Y., Okuno S., Kawai A., Shinomiya H., Saito A., Suzuki M.,
RA Omori Y., Nishino N., Kanemoto N., Fujiwara T., Horie M.,
RA Takahashi E.;
RT "Cloning and chromosomal mapping of a novel ABC transporter gene
RT (hABC7), a candidate for X-linked sideroblastic anemia with
RT spinocerebellar ataxia.";
RL J. Hum. Genet. 43:115-122(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98318631; PubMed=9653160;
RA Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,
RA He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,
RA Wang Y.-X., Chen S.-J., Chen Z.;
RT "Identification of genes expressed in human CD34(+) hematopoietic
RT stem/progenitor cells by expressed sequence tags and efficient full-
RT length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASAT MET-400.
RX MEDLINE=99214014; PubMed=10196363;
RA Allikmets R., Raskind W.H., Hutchinson A., Schueck N.D., Dean M.,
RA Koeller D.M.;
RT "Mutation of a putative mitochondrial iron transporter gene (ABC7) in
RT X-linked sideroblastic anemia and ataxia (XLSA/A).";
RL Hum. Mol. Genet. 8:743-749(1999).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASAT LYS-433.
RX MEDLINE=20504074; PubMed=11050011;
RA Bekri S., Kispal G., Lange H., Fitzsimons E., Tolmie J., Lill R.,
RA Bishop D.F.;
RT "Human ABC7 transporter: gene structure and mutation causing X-linked
RT sideroblastic anemia with ataxia with disruption of cytosolic
RT iron-sulfur protein maturation.";
RL Blood 96:3256-3264(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 5-752 FROM N.A.
RX MEDLINE=99098366; PubMed=9883897;
RA Csere P., Lill R., Kispal G.;
RT "Identification of a human mitochondrial ABC transporter, the
RT functional orthologue of yeast Atmlp.";
RL FEBS Lett. 441:266-270(1998).
CC -!- FUNCTION: COULD BE INVOLVED IN THE TRANSPORT OF HEME FROM THE
CC MITOCHONDRIA TO THE CYTOSOL. PLAYS A CENTRAL ROLE IN THE
CC MATURATION OF CYTOSOLIC IRON-SULFUR (FE/S) CLUSTER-CONTAINING
CC PROTEINS.
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -!- DISEASE: DEFECTS IN ABCB7 ARE THE CAUSE OF X-LINKED SIDEROBLASTIC
CC ANEMIA WITH ATAXIA (ASAT). ASAT IS A RECESSIVE DISORDER
CC CHARACTERIZED BY AN INFANTILE TO EARLY CHILDHOOD ONSET OF
CC NONPROGRESSIVE CEREBELLAR ATAXIA AND MILD ANEMIA WITH HYPOCHROMIA
CC AND MICROCYTOSIS.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC
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DR EMBL; AB005289; BAA28861.1; -
DR EMBL; AF038950; AAC39865.1; -
DR EMBL; AF133659; AAD33045.1; -
DR EMBL; AF241887; AAK20173.1; -
DR EMBL; AF241872; AAK20173.1; JOINED.
DR EMBL; AF241873; AAK20173.1; JOINED.
DR EMBL; AF241874; AAK20173.1; JOINED.
DR EMBL; AF241875; AAK20173.1; JOINED.
DR EMBL; AF241876; AAK20173.1; JOINED.
DR EMBL; AF241877; AAK20173.1; JOINED.
DR EMBL; AF241878; AAK20173.1; JOINED.
DR EMBL; AF241879; AAK20173.1; JOINED.
DR EMBL; AF241880; AAK20173.1; JOINED.
DR EMBL; AF241881; AAK20173.1; JOINED.
DR EMBL; AF241882; AAK20173.1; JOINED.
DR EMBL; AF241883; AAK20173.1; JOINED.
DR EMBL; AF241884; AAK20173.1; JOINED.
DR EMBL; AF241885; AAK20173.1; JOINED.
DR EMBL; AF241886; AAK20173.1; JOINED.
DR EMBL; BC006323; AAH06323.1; -
DR EMBL; AF078777; AAD47141.1; -
DR Genew; HGNC:48; ABCB7.
DR MIM; 300135; -
DR MIM; 301310; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranprtTM.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transmembrane; Transport; Mitochondrion; Inner membrane;
KW Transit peptide; Disease mutation.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 752 ATP-BINDING CASSETTE, SUB-FAMILY B, MEMBER 7.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 291 311 POTENTIAL.
FT TRANSMEM 383 403 POTENTIAL.
FT NP_BIND 505 512 ATP (POTENTIAL).
FT VARIANT 400 400 I -> M (IN ASAT).
FT VARIANT 433 433 /FTid=VAR_009156.
FT IMPAIRED MATURATION OF CYTOSOLIC FE/S PROTEINS).
FT /FTid=VAR_012640.
FT Q -> QQ (IN REF. 5).
FT A -> P (IN REF. 2).
FT R -> K (IN REF. 1).
FT LLPIMP -> PLPNHV (IN REF. 2).
FT V -> LV (IN REF. 2).
FT G -> C (IN REF. 2).
FT FALVT -> LLGN (IN REF. 2).
FT R -> G (IN REF. 1).
FT IEMNK -> LEIDQ (IN REF. 2).
FT F -> I (IN REF. 1).
FT E -> V (IN REF. 6).
SQ SEQUENCE 752 AA; 82641 MW; B1FFA57ABD24FB90 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 752;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 635 ATSSLDS 641
RESULT 5
MDR_PLAFF STANDARD; PRT; 1419 AA.
ID MDR_PLAFF
AC P13568;
DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multidrug resistance protein (Chloroquine resistance protein).
GN MDR1.
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89288297; PubMed=2701941;
RA Foote S.J., Thompson J.K., Cowman A.F., Kemp D.J.;
RT "Amplification of the multidrug resistance gene in some chloroquine-
resistant isolates of P. falciparum.";
RL Cell 57:921-930(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92017800; PubMed=1922044;
RA Triglia T., Foote S.J., Kemp D.J., Cowman A.F.;
RT "Amplification of the multidrug resistance gene pfmdr1 in Plasmodium
falciparum has arisen as multiple independent events.";
RL Mol. Cell. Biol. 11:5244-5250(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149200; PubMed=8426608;
RA Wilson C.M., Volkman S.K., Thaithong S., Martin R.K., Kyle D.E.,
RA Milhous W.K., Wirth D.F.;
RT "Amplification of pfmdr1 associated with mefloquine and halofantrine
resistance in Plasmodium falciparum from Thailand.";
RL Mol. Biochem. Parasitol. 57:151-160(1993).
CC -!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED
CC DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: P. FALCIPARUM RESISTANT TO THE DRUG CHLOROQUINE
CC -!- HAVE MULTIPLE COPIES OF THE GENE CODING FOR MDR.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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CC -----
DR EMBL; M29154; AAA29646.1; -;
DR EMBL; X56851; CAA40180.1; -;
DR EMBL; S53996; AAD13870.1; -;
DR PIR; A32547; DVZQF.
DR PIR; S18204; S18204.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranprtrTM.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transportr; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 82 POTENTIAL.
FT TRANSMEM 91 116 POTENTIAL.
FT TRANSMEM 160 188 POTENTIAL.
FT TRANSMEM 194 212 POTENTIAL.
FT TRANSMEM 279 298 POTENTIAL.
FT TRANSMEM 314 338 POTENTIAL.
FT DOMAIN 339 788 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 789 807 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 908 928 POTENTIAL.
FT TRANSMEM 1028 1048 POTENTIAL.
FT TRANSMEM 1063 1083 POTENTIAL.
FT DOMAIN 1084 1419 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 643 661 POLY-ASN.

FT NP_BIND 413 420 ATP (POTENTIAL).
FT NP_BIND 1161 1168 ATP (POTENTIAL).
FT REPEAT 1 721
FT REPEAT 722 1419
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1419 AA; 162251 MW; 0F96C7C1850B33D0 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 1419;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 1338 ATSSLDS 1344

RESULT 6
SON_MOUSE STANDARD; PRT; 2404 AA.
AC Q9QX47; Q9QXP5; Q9CQK6; Q9CQ12;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SON protein.
GN SON.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=129/Sv;
RX MEDLINE=20408886; PubMed=10950926;
RA Wynn S.L., Fisher R.A., Pagel C., Price M., Liu Q.Y., Khan I.M.,
RA Zammit P., Dadrah K., Mazrani W., Kessling A., Lee J.S., Buluwela L.;
RT "Organization and conservation of the GART/SON/DONSON locus in mouse
and human genomes.";
RL Genomics 68:57-62(2000).
RN [2]
RP SEQUENCE OF 1-116 FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Hippocampus, Small intestine, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Transcriptional repressor. Binds to the consensus DNA
CC sequence: 5'-GA[GT]AN[CG]AG[CC]-3'. Might protect cells from
CC apoptosis. Might be involved in pre-mRNA splicing (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- DOMAIN: Contains 8 types of repeats which are distributed in 3
CC regions.

CC -!- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
CC -----
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CC -----
DR EMBL; AF193606; AAF23120.1; -
DR EMBL; AF193595; AAF23120.1; JOINED.
DR EMBL; AF193596; AAF23120.1; JOINED.
DR EMBL; AF193597; AAF23120.1; JOINED.
DR EMBL; AF193598; AAF23120.1; JOINED.
DR EMBL; AF193599; AAF23120.1; JOINED.
DR EMBL; AF193600; AAF23120.1; JOINED.
DR EMBL; AF193601; AAF23120.1; JOINED.
DR EMBL; AF193602; AAF23120.1; JOINED.
DR EMBL; AF193603; AAF23120.1; JOINED.
DR EMBL; AF193604; AAF23120.1; JOINED.
DR EMBL; AF193605; AAF23120.1; JOINED.
DR EMBL; AF193607; AAF23121.1; -
DR EMBL; AK019312; BAB31659.1; -
DR EMBL; AK019081; BAB31536.1; -
DR EMBL; AK008478; BAB25691.1; -
DR EMBL; AK008256; BAB25562.1; -
DR MGD; MGI:98353; Son.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR000467; G_patch.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF01585; G-patch; 1.
DR SMART; SM00443; G-patch; 1.
DR PROSITE; PS0137; DS_RBD; 1.
DR PROSITE; PS50174; G_PATCH; 1.
KW RNA-binding; DNA-binding; Nuclear protein; Repeat;
KW Alternative splicing.
FT DOMAIN 721 850 13 X 10 AA TANDEM REPEATS OF L-A-[ST]-
[NSG]-[TS]-MDSQM.
FT DOMAIN 867 943 11 X 7 AA TANDEM REPEATS OF [DR]-P-Y-R-
[LI][AG][OHP].
FT DOMAIN 961 1080 14 X 6 AA REPEATS OF [ED]-R-S-M-M-S.
FT REPEAT 961 966 1-1.
FT REPEAT 969 974 1-2.
FT REPEAT 976 981 1-3.
FT REPEAT 985 990 1-4.
FT REPEAT 993 998 1-5.
FT REPEAT 1001 1006 1-6.
FT REPEAT 1010 1015 1-7.
FT REPEAT 1018 1023 1-8.
FT REPEAT 1026 1031 1-9.
FT REPEAT 1035 1040 1-10.
FT REPEAT 1044 1049 1-11.
FT REPEAT 1055 1060 1-12.
FT REPEAT 1066 1071 1-13.
FT REPEAT 1075 1080 1-14.
FT DOMAIN 1101 1133 3 X 11 AA TANDEM REPATS OF P-P-L-P-P-E-E-
P-P-[TME]-[MTG].
FT DOMAIN 1910 1979 7 X 7 AA REPEATS OF P-S-R-R-S-R-[TS].
FT REPEAT 1910 1916 2-1.
FT REPEAT 1938 1944 2-2.
FT REPEAT 1945 1951 2-3.
FT REPEAT 1952 1958 2-4.
FT REPEAT 1959 1965 2-5.
FT REPEAT 1966 1972 2-6.
FT REPEAT 1973 1979 2-7 (APPROXIMATE).
FT DOMAIN 1919 1990 2 X 19 AA REPEATS OF P-S-R-R-R-S-R-S-V-
V-R-R-R-S-F-S-I-S.
FT REPEAT 1919 1937 3-1.
FT REPEAT 1980 1990 3-2 (APPROXIMATE).
FT DOMAIN 1991 2017 3 X TANDEM REPEATS OF [ST]-P-[VLI]-R-
[RL]-[RK]-[RF]-S-R.

FT DOMAIN 2283 2329 G-PATCH.
FT DOMAIN 2349 2404 DRBM.
FT VARSPLIC 2086 2086 K -> F (IN ISOFORM 2).
FT VARSPLIC 2087 2404 MISSING (IN ISOFORM 2).
SQ SEQUENCE 2404 AA; 261428 MW; 648BF28ED3FC01D9 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 2404;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLDS 7
Db 802 ATSSMDS 808

RESULT 7
SON_HUMAN
ID SON_HUMAN STANDARD; PRT; 2426 AA.
AC P18583; O95981; Q9UPY0; Q14120; O14487; Q9UKP9; Q9H7B1; Q9P070;
AC Q9P072;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SON protein (SON3) (Negative regulatory element-binding protein) (NRE-
binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1)
DE (BASS1) (Protein C21orf50).
GN SON OR NREBP OR DBP5 OR C21ORF50 OR KIAA1019.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D; E AND F).
RX MEDLINE=21564202; PubMed=11707072;
RA Raymond A., Friedli M., Neergaard Henriksen C., Chapot F.,
RA Deutsch S., Ucla C., Rossier C., Lyle R., Guipponi M.,
RA Antonarakis S.E.;
RT "From PREDs and open reading frames to cDNA isolation: revisiting the
human chromosome 21 transcription map.";
RL Genomics 78:46-54(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM G).
RC TISSUE=Liver;
RX MEDLINE=21316479; PubMed=11306577;
RA Sun C.-T., Lo W.-Y., Wang I.-H., Lo Y.-H., Shiou S.-R., Lai C.-K.,
RA Ting L.-P.;
RT "Transcription repression of human hepatitis B virus genes by negative
regulatory element-binding protein/SON.";
RL J. Biol. Chem. 276:24059-24067(2001).
RN [3]
RP SEQUENCE OF 1-689 FROM N.A. (ISOFORM H).
RC TISSUE=Placenta;
RA Casadei R., Strippoli P., D'Addabbo P., Canaider S., Lenzi L.,
RA Vitale L., Giannone S., Carinci P., Zannotti M.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-130 FROM N.A.
RC TISSUE=Smooth muscle;
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-114 FROM N.A.
RC TISSUE=Blood;
RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [6]

Best Local Similarity 85.7%; Pred. No. 1.3e+02; Indels 0; Gaps 0; Matches 6; Conservative 1; Mismatches 0;

QY 1 ATSSLDS 7
|||||
Db 827 ATSSMDS 833

RESULT 8
LMRA_LACLA STANDARD; PRT; 584 AA.
ID LMRA_LACLA Q9CHL8;
AC 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding and permease protein.
DE LMRA OR LL0711.
GN Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OC NCBI_TaxID=1360;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=IL1403;
RC MEDLINE=21235186; PubMed=11337471;
RX Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RA "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
CC -!- FUNCTION: Efflux transporter for a variety of amphiphilic cationic
CC compounds, including antibiotics (By similarity).
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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EMBL; AE006305; AAK04809.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranprtTM.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Transmembrane; Antibiotic resistance;
KW Complete proteome.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 144 164 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
FT TRANSMEM 255 275 POTENTIAL.
FT TRANSMEM 286 306 POTENTIAL.
FT NP_BIND 376 383 ATP (POTENTIAL).
SQ SEQUENCE 584 AA; 63999 MW; 89F13E5926410462 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 584;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
|||||
Db 507 ATASLDS 513

RESULT 9
LMRA_LACLC STANDARD; PRT; 584 AA.
ID LMRA_LACLC P97046;
AC 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding and permease protein.
DE LMRA.
GN Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG1363;
RX MEDLINE=97008061; PubMed=8855237;
RA van Veen H.W., Venema K., Bolhuis H., Oussenko I., Kok J., Poolman B.,
RA Driessen A.J., Konings W.N.;
RT "Multidrug resistance mediated by a bacterial homolog of the human
RT multidrug transporter MDR1.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10668-10672(1996).
CC -!- FUNCTION: Efflux transporter for a variety of amphiphilic cationic
CC compounds, including antibiotics.
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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CC -----

EMBL; U63741; AAB49750.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranprtTM.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Transmembrane; Antibiotic resistance.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 144 164 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
FT TRANSMEM 255 275 POTENTIAL.
FT TRANSMEM 286 306 POTENTIAL.
FT NP_BIND 376 383 ATP (POTENTIAL).
SQ SEQUENCE 584 AA; 63918 MW; C8E1CD9469C3A725 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 584;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 507 ATASLDS 513

RESULT 10
Y4GM_RHISN STANDARD; PRT; 586 AA.
ID Y4GM_RHISN AC P55469;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ABC transporter ATP-binding protein Y4GM.
GN Y4GM.

```
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
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CC -----
DR EMBL; AE000075; AAB91687.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranprtrTM.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Hypothetical protein; ATP-binding; Transport; Transmembrane; Plasmid.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 56 86 POTENTIAL.
FT TRANSMEM 152 172 POTENTIAL.
FT TRANSMEM 256 276 POTENTIAL.
FT NP_BIND 379 386 ATP (POTENTIAL).
SQ SEQUENCE 586 AA; 64262 MW; 1095DFEB82620637 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 586;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 509 ATSALDS 515

RESULT 11
HEPA_ANASP
ID HEPA_ANASP STANDARD; PRT; 607 AA.
AC P22638;
DT 01-AUG-1991 (Rel. 19, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heterocyst differentiation ATP-binding protein hepa.
GN HEPA OR HETA OR ALR2835.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264305; PubMed=2111805;
RA Holland D., Wolk C.P.;
RT "Identification and characterization of hetaA, a gene that acts early
RT in the process of morphological differentiation of heterocysts.";
RL J. Bacteriol. 172:3131-3137(1990).
RN [2]
RP REVISIONS.
RA Zhu J., Wolk C.P.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -!- FUNCTION: ACTS EARLY IN THE PROCESS OF MORPHOLOGICAL
CC DIFFERENTIATION OF HETEROCYSTS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- INDUCTION: BY DEPRIVATION OF NITRATE.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF031959; AAC32400.1; ALT_INIT.
DR EMBL; AP003591; BAB74534.1; -.
DR PIR; A35391; A35391.
DR HSSP; P13569; INBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranprtrTM.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Heterocyst; ATP-binding; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 88 110 POTENTIAL.
FT TRANSMEM 163 182 POTENTIAL.
FT TRANSMEM 186 208 POTENTIAL.
FT TRANSMEM 285 307 POTENTIAL.
FT NP_BIND 397 404 ATP (POTENTIAL).
SQ SEQUENCE 607 AA; 67789 MW; B47970D4758F564F CRC64;

Query Match 90.3%; Score 28; DB 1; Length 607;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 527 ATSALDS 533

RESULT 12
YA51_HAEIN
ID YA51_HAEIN STANDARD; PRT; 614 AA.
AC Q57180; O05043;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein HI1051.
GN HI1051.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
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RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
CC -----
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CC -----
DR EMBL: U32785; AAC22709.1; -.
DR TIGR: H11051; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001140; ABCtranprtTM.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF00664; ABC_membrane; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW Hypothetical protein; ATP-binding; Transport; Transmembrane;
KW Complete proteome.
FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 157 177 POTENTIAL.
FT TRANSMEM 178 198 POTENTIAL.
FT NP_BIND 397 404 ATP (POTENTIAL).
SQ SEQUENCE 614 AA; 68398 MW; 306BBA9546921EA0 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 614;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLDS 7
Db 532 ATSALDS 538
|||:||||

RESULT 13
MDL1_CANAL
ID MDL1_CANAL STANDARD; PRT; 685 AA.
AC P97998;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP-dependent permease MDL1.
GN MDL1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=491A;
RA McCreath K.J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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CC -----
DR EMBL: Y12327; CAA72996.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001140; ABCtranprtTM.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF00664; ABC_membrane; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transmembrane; Glycoprotein; Transport.
FT TRANSMEM 96 116 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 256 276 POTENTIAL.
FT TRANSMEM 354 374 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT NP_BIND 475 482 ATP (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 576 576 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 685 AA; 75868 MW; 46239E214CE1267A CRC64;

Query Match 90.3%; Score 28; DB 1; Length 685;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLDS 7
Db 606 ATSALDS 612
|||:||||

RESULT 14
MDL1_YEAST
ID MDL1_YEAST STANDARD; PRT; 695 AA.
AC P33310;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-dependent permease MDL1.
GN MDL1 OR YLR188W OR L9470.3.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94287714; PubMed=7912468;
RA Dean M.C., Allikmets R., Gerrard B.C., Stewart C., Kistler A.,
RA Shfer B., Michaelis S., Strathern J.;
RT "Mapping and sequencing of two yeast genes belonging to the
RT ATP-binding cassette superfamily.";
RL Yeast 10:377-383(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=9713267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kottler P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelie D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 5.58621 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	42	89.4	130	1	KV5G_MOUSE	P01639 mus musculu
2	37	78.7	128	1	KV3K_HUMAN	P06311 homo sapien
3	36	76.6	282	1	PSTA_HAEIN	P45190 haemophilus
4	36	76.6	947	1	PM19_CHLPN	Q92813 chlamydia p
5	35	74.5	108	1	KV3A_HUMAN	P01619 homo sapien
6	35	74.5	117	1	KV5H_MOUSE	P01641 mus musculu
7	35	74.5	1897	1	PTPF_HUMAN	P10586 homo sapien
8	34	72.3	129	1	KV3M_HUMAN	P18136 homo sapien
9	34	72.3	131	1	Y15K_WDV	P06848 wheat dwarf
10	34	72.3	250	1	QCRC_BACST	Q45659 bacillus st
11	34	72.3	287	1	PSTA_XYLFA	Q9pbk1 xylella fas
12	34	72.3	461	1	DCUC_ECOLI	Q47134 escherichia
13	33	70.2	108	1	KV1R_HUMAN	P01610 homo sapien
14	33	70.2	351	1	RNFD_YERPE	Q8zed2 versinia pe
15	32	68.1	108	1	KV1O_HUMAN	P01607 homo sapien
16	32	68.1	128	1	YC35_CYAPA	P48275 cyanophora
17	32	68.1	527	1	VG12_BPT4	P10930 bacteriopho
18	32	68.1	552	1	MCRA_METJA	Q60391 methanococc
19	32	68.1	658	1	LYTB_STRPN	Q9z4p7 streptococc
20	32	68.1	854	1	SBP2_HUMAN	Q96t21 homo sapien
21	32	68.1	2244	1	PYR1_SCHPO	Q09794 schizosacch
22	31	66.0	85	1	Y12K_MSVS	P14993 maize strea
23	31	66.0	108	1	KV1V_HUMAN	P04430 homo sapien
24	31	66.0	109	1	KV3B_HUMAN	P01620 homo sapien
25	31	66.0	352	1	RNFD_ECO57	P58325 escherichia
26	31	66.0	352	1	RNFD_ECOLI	P76182 escherichia
27	31	66.0	352	1	RNFD_SALTY	Q8z6q8 salmonella
28	31	66.0	352	1	RNFD_SALTY	Q8zpm3 salmonella
29	31	66.0	470	1	VL2_HPV54	Q81023 human papil
30	31	66.0	497	1	SPK1_DUGTI	P42687 dugesia tig
31	31	66.0	511	1	EGR1_BRARE	P26632 brachydanio
32	31	66.0	556	1	C4G1_DROME	Q9v3s0 drosophila
33	31	66.0	565	1	HXB1_HAEIN	P44601 haemophilus

34	31	66.0	565	1	HXB2_HAEIN	P45356 haemophilus
35	31	66.0	1912	1	PTPD_HUMAN	P23468 homo sapien
36	30	63.8	109	1	KV3D_HUMAN	P01622 homo sapien
37	30	63.8	114	1	KV4A_HUMAN	P01625 homo sapien
38	30	63.8	209	1	P1MT_HELPJ	Q9zkc2 helicobacte
39	30	63.8	209	1	P1MT_HELPY	P56133 helicobacte
40	30	63.8	271	1	AQP2_MOUSE	P56402 mus musculu
41	30	63.8	271	1	AQP2_RAT	P34080 rattus norv
42	30	63.8	306	1	DDL_BUCAP	O51927 buchnera ap
43	30	63.8	308	1	DDL_AGRT5	Q8udn3 agrobacteri
44	30	63.8	345	1	NUOH_RHOCA	P42032 rhodobacter
45	30	63.8	404	1	THII_STRPN	Q97rel streptococc

ALIGNMENTS

RESULT 1						
KV5G_MOUSE						
ID	KV5G_MOUSE	STANDARD;	PRT;	130	AA.	
AC	P01639; P01640;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Ig kappa chain V-V region MOPC 41 precursor.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=79221900; PubMed=111146;					
RA	Seidman J.G., Max E.E., Leder P.;					
RT	"A kappa-immunoglobulin gene is formed by site-specific recombination					
RT	without further somatic mutation.";					
RL	Nature 280:370-375(1979).					
RN	[2]					
RP	SEQUENCE OF 1-33.					
RX	MEDLINE=77148916; PubMed=403522;					
RA	Burstein Y., Schechter I.;					
RT	"Amino acid sequence of the NH2-terminal extra piece segments of the					
RT	precursors of mouse immunoglobulin lambda1-type and kappa-type light					
RT	chains.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).					
RN	[3]					
RP	SEQUENCE OF 23-130.					
RX	MEDLINE=67056897; PubMed=4162931;					
RA	Gray W.R., Dreyer W.J., Hood L.;					
RT	"Mechanism of antibody synthesis: size differences between mouse					
RT	kappa chains.";					
RL	Science 155:465-467(1967).					
CC	-!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE					
CC	SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.					
CC	-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.					
DR	PIR; A01922; KVM5M4.					
DR	HSSP; P01607; 1REI.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR003596; Ig_v.					
DR	Pfam; PF00047; Ig; 1.					
DR	SMART; SM00406; IGV; 1.					
KW	Immunoglobulin V region; Signal; Bence-Jones protein.					
FT	SIGNAL 1 22					
FT	CHAIN 23 130					
FT	DOMAIN 23 45					
FT	DOMAIN 46 56					
FT	DOMAIN 57 71					
FT	DOMAIN 72 78					
FT	DOMAIN 79 110					
FT	DOMAIN 111 119					
FT	DOMAIN 120 129					
FT	DISULFID 45 110					
FT	DI VARIANT 1 2					
FT	NON_TER 130 130					

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SQ SEQUENCE 130 AA; 14311 MW; 5EFE0FE71D5F1BEC CRC64;
Query Match 89.4%; Score 42; DB 1; Length 130;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYASSPYT 9
|||||:|
Db 111 QYASSPWT 119

RESULT 2
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;
Query Match 78.7%; Score 37; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|||||
Db 110 QYSTSPYT 117

RESULT 3
PSTA_HAEIN STANDARD; PRT; 282 AA.
ID PSTA_HAEIN
AC P45190;
```

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphate transport system permease protein pstA.
GN PSTA OR H11381.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Spriggs D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.
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CC -----
DR EMBL; U32818; AAC23026.1; -.
DR TIGR; H11381; -.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
DR TIGRFAMS; TIGR00974; 3a0107s02c; 1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
KW Transport; Phosphate transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 20 42 POTENTIAL.
FT TRANSMEM 70 92 POTENTIAL.
FT TRANSMEM 111 133 POTENTIAL.
FT TRANSMEM 138 157 POTENTIAL.
FT TRANSMEM 197 219 POTENTIAL.
FT TRANSMEM 256 278 POTENTIAL.
SQ SEQUENCE 282 AA; 31194 MW; 16D9907FB1256112 CRC64;
Query Match 76.6%; Score 36; DB 1; Length 282;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|||||:|
Db 243 QYAAASPFT 250

RESULT 4
PM19_CHLPN STANDARD; PRT; 947 AA.
ID PM19_CHLPN
AC Q9Z813; Q9JSE2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```


DE Probable outer membrane protein pmp19 precursor (Polymorphic membrane
DE protein 19).
GN PMP19 OR CPN0539 OR CP0213.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RA "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RT Nat. Genet. 21:385-389(1999).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20298986; PubMed=10839753;
RA Shirai M., Hirakawa H., Ouchi K., Tabuchi M., Kishi F., Kimoto M.,
RA Takeuchi H., Nishida J., Shibata K., Fujinaga R., Yoneda H.,
RA Matsushima H., Tanaka C., Furukawa S., Miura K., Nakazawa A.,
RA Ishii K., Shiba T., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of outer membrane protein genes omp and pmp in the whole
RT genome sequences of Chlamydia pneumoniae isolates from Japan and the
RT United States.";
RL J. Infect. Dis. 181 Suppl 3:S524-S527(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.

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EMBL; AE001638; AAD18679.1; -.
EMBL; AE002181; AAF38083.1; -.
EMBL; AP002547; BAA98745.1; -.
HSSP; Q90121; 1KPT.
TIGR; CP0213; -.
InterPro; IPR003368; Chlamydia_PMP.
InterPro; IPR003357; OMP.
Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 1.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 947 PROBABLE OUTER MEMBRANE PROTEIN PMP19.
FT CONFLICT 453 453 E -> D (IN REF. 3).
SQ SEQUENCE 947 AA; 103642 MW; 20CELDEEE1606DFF CRC64;

Query Match 76.6%; Score 36; DB 1; Length 947;
Best Local Similarity 75.0%; Pred. NO. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
:|||||
Db 560 EYASKPYT 567

RESULT 5

KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01891; K3HUB6.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 74.5%; Score 35; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. NO. 3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
:|||||
Db 91 QYGSSPFT 98

RESULT 6

KV5H_MOUSE STANDARD; PRT; 117 AA.
AC P01641;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 173B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81064681; PubMed=6777049;
RA Max E.E., Seidman J.G., Miller H., Leder P.;
RT "Variation in the crossover point of kappa immunoglobulin gene V-J
RT recombination: evidence from a cryptic gene.";
RL Cell 21:793-799(1980).
CC -----
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CC -----

DR EMBL; K00880; AAA39031.1; -.
DR PIR; A01924; KVMS3B.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 117 IG KAPPA CHAIN V-V REGION MOPC 173B.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12954 MW; 24B3D4B9AC2E4D6C CRC64;

Query Match 74.5%; Score 35; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYASSP 7
|||||
Db 111 QYASSP 117

RESULT 7
PTPE_HUMAN
ID PTPF_HUMAN STANDARD; PRT; 1897 AA.
AC P10586;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).
GN PTPRF OR LAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RX MEDLINE=89035978; PubMed=2972792;
RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;
RT "A new member of the immunoglobulin superfamily that has a
RT cytoplasmic region homologous to the leukocyte common antigen.";
RL J. Exp. Med. 168:1523-1530(1988).
RN [2]
RP MUTAGENESIS.
RX MEDLINE=90046860; PubMed=2554325;
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
RT "A family of receptor-linked protein tyrosine phosphatases in humans
RT and Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
RT domains of the receptor-linked protein tyrosine phosphatases LCA and
RT LAR.";
RL EMBO J. 9:2399-2407(1990).
CC -!- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.
CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
CC (PTPASE).
CC -!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE

CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC FIRST ONE.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O - protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC -----

DR EMBL; Y00815; CAA68754.1; -.
DR PIR; S03841; TDHULK.
DR HSSP; P18052; IYFO.
DR Genew; HGNC:9670; PTPRF.
DR MIM; 179590; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FnIII_repeat.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00041; fn3; 7.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00700; PRTYPHPHTASE.
DR SMART; SM00060; FN3; 5.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW Cell adhesion; Immunoglobulin domain; Repeat.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 1897 LAR PROTEIN.
FT DOMAIN 17 1250 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1251 1274 POTENTIAL.
FT DOMAIN 1275 1897 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1360 1606 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 1649 1897 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 1538 1538 BY SIMILARITY.
FT ACT_SITE 1829 1829 BY SIMILARITY.
FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 711 711 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 956 956 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 1538 1538 C->S: LOSS OF ACTIVITY.
SQ SEQUENCE 1897 AA; 211844 MW; 439850FID5C031FF CRC64;

Query Match 74.5%; Score 35; DB 1; Length 1897;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
:|||||:
Db 1226 QYASSPYS 1233

RESULT 8
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

Db 97 YASGPYT 103

RESULT 11

PSTA_XYLFA STANDARD; PRT; 287 AA.

ID Q9PBK1;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Phosphate transport system permease protein pstA.

GN PSTA OR XF2143.

OS Xylella fastidiosa.

OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

OC Xylella.

OX NCBI_TaxID=2371;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=9a5C;

RX MEDLINE=20365717; PubMed=10910347;

RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,

RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,

RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,

RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,

RA de Rosa V.E. Jr., de Sa R.G., Santeili R.V., Sawasaki H.E.,

RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,

RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchako M.H.,

RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;

RT "The genome sequence of the plant pathogen xylella fastidiosa.";

RL Nature 406:151-159(2000).

CC -!- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

CC FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE

CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

CC (By similarity).

CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT

CC SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.

CC -----

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CC -----

DR EMBL; AE004029; AAF84942.1; --.

DR InterPro; IPR000515; BPD_transp.

DR Pfam; PF00528; BPD_transp; 1.

DR TIGRFAMS; TIGR00974; 3a0107s02c; 1.

DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.

KW Transport; Phosphate transport; Transmembrane; Inner membrane;

KW Complete proteome.

FT TRANSMEM 20 42 POTENTIAL.

FT TRANSMEM 75 97 POTENTIAL.

FT TRANSMEM 109 131 POTENTIAL.

FT TRANSMEM 136 158 POTENTIAL.

FT TRANSMEM 190 212 POTENTIAL.

FT TRANSMEM 252 274 POTENTIAL.

SQ SEQUENCE 287 AA; 31060 MW; 1514AAG18630505A CRC64;

Query Match 72.3%; Score 34; DB 1; Length 287;

Best Local Similarity 85.7%; Pred. NO. 14;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPY 8

Db 244 QFASSPY 250

RESULT 12

DCUC_ECOLI STANDARD; PRT; 461 AA.

ID DCUC_ECOLI

AC Q47134; Q9ZBC9; Q9ZBD0;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Anaerobic C4-dicarboxylate transporter dcuC.

GN DCUC OR B0621 OR Z0766 OR ECS0660.

OS Escherichia coli, and

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562, 83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / AN387;

RX MEDLINE=97113548; PubMed=8955408;

RZ Zientz E., Six S., Unden G.;

RT "Identification of a third secondary carrier (DcuC) for anaerobic

RT C4-dicarboxylate transport in Escherichia coli: roles of the three

RT Dcu carriers in uptake and exchange.";

RL J. Bacteriol. 178:7241-7247(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,

RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,

RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.;

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / W3110;

RX MEDLINE=97061202; PubMed=8905232;

RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,

RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

RA Yano M., Horiuchi T.;

RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 12.7-28.0 min region on the linkage map.";

RL DNA Res. 3:137-155(1996).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;

RX MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [7]
RN FUNCTION.
RC STRAIN=K12 / AN387;
RX MEDLINE=99296581; PubMed=10368146;
RA Zientz E., Janausch I.G., Six S., Unden G.;
RT "Functioning of DcuC as the C4-dicarboxylate carrier during glucose
RT fermentation by Escherichia coli.";
RL J. Bacteriol. 181:3716-3720(1999).
CC -!- FUNCTION: RESPONSIBLE FOR THE TRANSPORT OF C4-DICARBOXYLATES
CC DURING ANAEROBIC GROWTH.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: BELONGS TO THE DCUC / DCUD (TC 2.A.61) FAMILY OF
CC TRANSPORTERS.
CC -!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO THE
CC PRESENCE OF AN IS5 INSERTION ELEMENT BETWEEN CODONS 327 AND 328.
CC STRAIN W3110A BUT NOT W3110B HARBORS THIS IS5 INSERTION.
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CC -----
CC EMBL; X99112; CAA67561.1; -.
CC EMBL; AE000167; AAC73722.1; -.
CC EMBL; U82598; AAB40821.1; -.
CC EMBL; D90703; BAA35264.1; ALT_TERM.
CC EMBL; D90703; BAA35263.1; ALT_INIT.
CC EMBL; D90702; BAA35257.1; ALT_INIT.
CC EMBL; AE005241; AAG54956.1; -.
CC EMBL; AP002552; BAB34083.1; -.
CC EcoGene; EG13545; dcuC.
CC InterPro; IPR004669; DcuC.
CC Pfam; PF03606; DcuC; 1.
CC TIGRFAMs; TIGR00771; DcuC; 1.
KW Transmembrane; Inner membrane; Transport; Complete proteome.
FT TRANSMEM 2 22 POTENTIAL.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 267 287 POTENTIAL.
FT TRANSMEM 313 333 POTENTIAL.
FT TRANSMEM 343 363 POTENTIAL.
FT TRANSMEM 436 456 POTENTIAL.
SQ SEQUENCE 461 AA; 48412 MW; D4042FBFE9F562ED CRC64;

Query Match 72.3%; Score 34; DB 1; Length 461;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYASSPY 8
Db 110 LOYINSPY 117
RESULT 13
KVIR_HUMAN
ID KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHUWE.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
Query Match 70.2%; Score 33; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LOYASSPYT 9
Db 89 LOYSFPWT 97
RESULT 14
RNFD_YERPE
ID RNFD_YERPE STANDARD; PRT; 351 AA.
AC Q8ZED2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electron transport complex protein rnfd.
GN RNFD OR YPO2242.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebailhia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RA "Genome sequence of Yersinia pestis, the causative agent of plague";
RL Nature 413:523-527(2001).
CC -!- FUNCTION: May be part of a membrane complex involved in electron
CC transport (By similarity).
CC -!- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC,
CC rnfD, rnfE and rnfG (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: BELONGS TO THE NQR/RNFD FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ414151; CAC91048.1; -;
DR InterPro; IPR004338; NQR2_Rnfd_Rnfe.
DR Pfam; PF03116; NQR2_Rnfd_Rnfe; 1.
KW Electron transport; Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 21 43 POTENTIAL.
FT TRANSMEM 93 115 POTENTIAL.
FT TRANSMEM 122 144 POTENTIAL.
FT TRANSMEM 210 232 POTENTIAL.
FT TRANSMEM 237 259 POTENTIAL.
FT TRANSMEM 269 291 POTENTIAL.
FT TRANSMEM 298 315 POTENTIAL.
SQ SEQUENCE 351 AA; 38112 MW; A35BAE7524F605F8 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 351;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
: | | | | | | |
Db 1 MQIASSPFT 9

RESULT 15
KV10_HUMAN STANDARD; PRT; 108 AA.
ID KV10_HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;

RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01873; KIHURE.
DR PDB; 1REI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 68.1%; Score 32; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
: | | | | | | |
Db 90 QYQSLPYT 97

Search completed: March 10, 2003, 16:57:47
Job time : 6.58621 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 11.9483 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	88	2 PL0261	Ig kappa chain V r
2	42	77.8	106	2 PL0260	Ig kappa chain V r
3	42	77.8	130	1 KVMSM4	Ig kappa chain pre
4	38	70.4	114	2 S00996	Ig kappa chain pre
5	37	68.5	106	2 PL0259	Ig kappa chain V r
6	37	68.5	234	2 S38083	probable purine nu
7	36	66.7	305	2 AF0305	sugar binding prot
8	36	66.7	442	2 E71523	hypothetical prote
9	36	66.7	548	2 A86385	hypothetical prote
10	35	64.8	95	2 PH0867	Ig kappa chain V r
11	35	64.8	107	2 I69017	anti-HIV1 envelope
12	35	64.8	108	2 C30502	Ig kappa chain V r
13	34	63.0	193	2 H82028	hypothetical prote
14	34	63.0	252	2 S62431	40s ribosomal prot
15	34	63.0	269	2 H70179	spermidine/putresc
16	34	63.0	324	2 AE0554	probable oxidoredu
17	34	63.0	377	2 T05427	hypothetical prote
18	34	63.0	471	2 A81680	conserved hypothet
19	34	63.0	494	1 S22687	intercellular spre
20	34	63.0	876	2 G70863	probable valS prot
21	34	63.0	886	2 A87093	valyl-tRNA synthas
22	33	61.1	87	2 PH1082	Ig light chain V r
23	33	61.1	107	2 S32188	Ig kappa chain V r
24	33	61.1	115	1 KVMSL7	Ig kappa chain pre
25	33	61.1	117	2 S46376	Ig kappa chain V-J
26	33	61.1	128	2 PN0445	Ig kappa chain pre
27	33	61.1	129	2 B23986	Ig kappa chain pre
28	33	61.1	129	2 S29627	Ig kappa chain V r
29	33	61.1	129	2 S40332	Ig kappa chain - h

30	33	61.1	225	2 T03555	hypothetical prote
31	33	61.1	237	2 S65313	probable membrane
32	33	61.1	322	2 S35380	mcs2 protein - fis
33	33	61.1	346	2 T35215	hypothetical prote
34	33	61.1	349	2 D75419	proline dipeptidas
35	33	61.1	366	2 B95876	probable ABC trans
36	33	61.1	375	2 T25089	hypothetical prote
37	33	61.1	415	1 GRECS7	sucrose transport
38	33	61.1	415	2 A98034	sucrose transport
39	33	61.1	415	2 B85878	sucrose permease l
40	33	61.1	530	1 KICHPM	pyruvate kinase (E
41	33	61.1	548	2 JC6174	immunodominant 120
42	33	61.1	663	2 S67259	MNE1 protein - yea
43	33	61.1	666	2 F71310	probable periplasm
44	33	61.1	672	2 D81746	type III secretion
45	33	61.1	921	2 F71486	probable yopc/gen

ALIGNMENTS

RESULT 1
PL0261

Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C;Accession: PL0261

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0261

A;Molecule type: mRNA

A;Residues: 1-88 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-5/Region: framework 1

F;6-16/Region: complementarity-determining 1

F;17-31/Region: framework 2

F;32-38/Region: complementarity-determining 2

F;39-70/Region: framework 3

F;71-79/Region: complementarity-determining 3

F;80-88/Region: framework 4

Query Match 77.8%; Score 42; DB 2; Length 88;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10

Db 6 RASQDIGSSL 15

RESULT 2
PL0260

Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0260

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0260

A;Molecule type: mRNA

A;Residues: 1-106 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-90/Domain: immunoglobulin homology <IMM>

F;24-34/Region: complementarity-determining 1

F;35-49/Region: framework 2

F;50-56/Region: complementarity-determining 2

F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match 77.8%; Score 42; DB 2; Length 106;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 3
KVMSM4
Ig kappa chain precursor V region (MOPC 41) - mouse
N;Contains: Ig kappa chain precursor V region VK41
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999
C;Accession: A93211; A93211; A93815; A94239; A01922; A01923
R;Seidman, J.G.; Max, E.E.; Leder, P.
Nature 280, 370-375, 1979
A;Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu
A;Reference number: A93211; MUID:79221900; PMID:111146
A;Accession: A93211
A;Molecule type: DNA
A;Residues: 1-130 <PC41>
A;Accession: B93211
A;Molecule type: DNA
A;Residues: 1-117 <VK41>
A;Cross-references: GB:J00804; GB:J00566; NID:g52127; PIDN:CAA24186.1; PID:g575660
A;Note: the sequences were determined from the differentiated gene MOPC 41 and the germli
R;Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Accession: A93815
A;Molecule type: protein
A;Residues: 1-33 <BUR>
A;Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
R;Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A;Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.
A;Reference number: A94239; MUID:67056897; PMID:4162931
A;Accession: A94239
A;Molecule type: protein
A;Residues: 23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'BZ',65-76,'B',78-108,110-130 <GRA>
A;Experimental source: Bence Jones protein MOPC 41
C;Genetics:
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: alternative initiators; heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status experimental <SIG1>
F;3-22/Domain: signal sequence #status experimental <SIG2>
F;23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

Query Match 77.8%; Score 42; DB 1; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 46 RASQDIGSSL 55

RESULT 4
S00996
Ig kappa chain precursor V region (A10) - human (fragment)
C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
C;Accession: S00996
R;Straubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.
Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
A;Title: Two unusual human immunoglobulin V-kappa genes.
A;Reference number: S00996; MUID:89134397; PMID:2852016
A;Accession: S00996
A;Molecule type: DNA
A;Residues: 1-114 <STR>
A;Cross-references: EMBL:M27750; NID:g185914; PIDN:AAA58912.1; PID:g553479
A;Note: this sequence was determined from the germline gene
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-114/Product: Ig kappa chain V region #status predicted <MAT>
F;42-107/Disulfide bonds: #status predicted

Query Match 70.4%; Score 38; DB 2; Length 114;
Best Local Similarity 72.7%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
| | | | | | | |
Db 43 RASQSIGSSLH 53

RESULT 5
PL0259
Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0259
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0259
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match 68.5%; Score 37; DB 2; Length 106;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGRSL 33

RESULT 6
S38083
probable purine nucleotide-binding protein YPT52 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKR014c
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: S38083
R;Duesterhoeft, A.; Moestl, D.; Poehlmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37811
A;Accession: S38083
A;Molecule type: DNA

A;Residues: 1-234 <DUE>
A;Cross-references: EMBL:Z28239; NID:g486428; PIDN:CAA82086.1; PID:g486429; MIPS:YKR0140
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:YPT52
A;Cross-references: SGD:S0001722; MIPS:YKR014c
A;Map position: 11R
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; P-loop; purine nucleotide binding
F;10-17/Region: nucleotide-binding motif A (P-loop)
F;125-128/Region: GTP-binding NKXD motif
F;175-177/Region: GTP-binding SAK/L motif
F;16/Binding site: ATP/GTP (Lys) #status predicted

Query Match 68.5%; Score 37; DB 2; Length 234;
Best Local Similarity 87.5%; Pred. No. 6.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QDIGSKLY 11
|||||
Db 187 QDIGEKLY 194

RESULT 7
AF0305
sugar binding protein precursor [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0305
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0305
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC91306.1; PID:gl5980495; GSPDB:GN00175
C;Genetics:
A;Gene: rbsB

Query Match 66.7%; Score 36; DB 2; Length 305;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
:|: |||:|:
Db 52 QAANDIGAKVY 62

RESULT 8
E71523
hypothetical protein CT372 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: E71523
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71523
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-442 <ARN>
A;Cross-references: GB:AE001310; GB:AE001273; NID:g3328789; PIDN:AAC67968.1; PID:g332879
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT372

Query Match 66.7%; Score 36; DB 2; Length 442;
Best Local Similarity 80.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
||| | |||
Db 327 ASQHISSKLY 336

RESULT 9
A86385
hypothetical protein F2J7.18 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: A86385
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86385
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-548 <STO>
A;Cross-references: GB:AE005172; NID:g10092315; PIDN:AAG12726.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 548;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
:|: |||:|:
Db 48 KALYDIGAKLY 58

RESULT 10
PH0867
Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0867
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0867
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

Query Match 64.8%; Score 35; DB 2; Length 95;
Best Local Similarity 72.7%; Pred. No. 6.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
||| | |||
Db 24 RASQSIGSFLH 34

RESULT 11
I69017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (f
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I69017
R;Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A;Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A;Reference number: I54563; MUID:95237884; PMID:7721339
A;Accession: I69017
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-107 <RES>
A;Cross-references: GB:S77140; NID:9913352; PIDN:AAB34102.1; PID:g913353
C;Genetics:
A;Gene: Ig Vkappa
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 35; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
||| |||| I
Db 24 RASHDIGSYL 33

RESULT 12
C30502
Ig kappa chain V region (D444) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: C30502
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: C30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <EIL>
A;Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 35; DB 2; Length 108;
Best Local Similarity 63.6%; Pred. No. 7.5;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
|||| ||: I:
Db 24 RASQSIGTSLH 34

RESULT 13
H82028
hypothetical protein NMA0330 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H82028
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H82028
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <PAR>

A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83635.1; PID:g737
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA0330

Query Match 63.0%; Score 34; DB 2; Length 193;
Best Local Similarity 63.6%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
||:| |:|||
Db 63 RAAQKRGAKLY 73

RESULT 14
S62431
40s ribosomal protein s3ae (S1) - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: protein SPAC13G6.02c
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 10-Dec-1999
C;Accession: S62431; T37637
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, October 1995
A;Reference number: S62430
A;Accession: S62431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <ODE>
A;Cross-references: EMBL:Z54308; NID:g1008985; PIDN:CAA91095.1; PID:g1008987
R;Odell, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21734
A;Accession: T37637
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-252 <OD2>
A;Cross-references: EMBL:Z54308; PIDN:CAA91095.1; GSPDB:GN00066; SPDB:SPAC13G6.02c
A;Experimental source: strain 972h-; cosmid cl3G6
C;Genetics:
A;Gene: rps1-1
A;Map position: 1L
C;Superfamily: rat ribosomal protein S3a
C;Keywords: protein biosynthesis; ribosome

Query Match 63.0%; Score 34; DB 2; Length 252;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
|||:|||:
Db 235 SQDVGSKV 242

RESULT 15
H70179
spermidine/putrescine ABC transporter, permease protein (potB) homolog - Lyme disease
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 24-Sep-1999
C;Accession: H70179
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70179
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-269 <KLE>
A;Cross-references: GB:AE001165; GB:AE000783; NID:g2688561; PIDN:AAB91526.1; PID:g268
A;Experimental source: strain B31
C;Superfamily: spermidine/putrescine transport system permease protein potH

Query Match 63.0%; Score 34; DB 2; Length 269;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
|||||:
Db 171 ASQDLGARMW 180

Search completed: March 10, 2003, 17:01:22
Job time : 13.9483 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 7.60345 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	88	2	PL0261 Ig kappa chain V r
2	31	100.0	106	2	PL0260 Ig kappa chain V r
3	31	100.0	106	2	PL0259 Ig kappa chain V r
4	31	100.0	130	1	KVMSM4 Ig kappa chain pre
5	31	100.0	131	2	E97737 hypothetical prote
6	31	100.0	320	2	AI3469 ABC transporter AT
7	31	100.0	548	2	F71732 ABC transporter AT
8	31	100.0	555	2	S63137 hypothetical prote
9	31	100.0	589	2	D70031 ABC transporter (A
10	31	100.0	589	2	F97735 hypothetical prote
11	31	100.0	600	2	AD3138 hypothetical prote
12	31	100.0	600	2	H98149 ATP-binding transp
13	31	100.0	604	2	S60182 ATP-binding transp
14	31	100.0	604	2	H95974 msbA-like sacchari
15	31	100.0	1025	2	T18376 multidrug resistan
16	31	100.0	1419	1	DVZQF multidrug resist
17	28	90.3	327	2	H64716 ABC transporter, A
18	28	90.3	327	2	F71800 ABC transporter, A
19	28	90.3	428	2	T43532 zinc finger protei
20	28	90.3	534	2	S77239 ABC-type transport
21	28	90.3	546	2	AG1886 ATP-binding protei
22	28	90.3	571	2	S58356 pepT protein - Sta
23	28	90.3	575	2	AB1793 ABC transporter (A
24	28	90.3	575	2	AH1417 ABC transporter (A
25	28	90.3	578	2	A83739 ABC transporter (A
26	28	90.3	584	2	G86713 hypothetical prote
27	28	90.3	587	2	C98165 probable ABC trans
28	28	90.3	587	2	AD3122 hypothetical prote
29	28	90.3	588	2	A75282 ABC transporter, A

ALIGNMENTS

RESULT 1

PL0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C;Accession: PL0261
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0261
A;Molecule type: mRNA
A;Residues: 1-88 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-5/Region: framework 1
F;6-16/Region: complementarity-determining 1
F;17-31/Region: framework 2
F;32-38/Region: complementarity-determining 2
F;39-70/Region: framework 3
F;71-79/Region: complementarity-determining 3
F;80-88/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 32 ATSSLDS 38

RESULT 2

PL0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment) ;
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0260
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0260
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2

F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 50 ATSSLDS 56

RESULT 3
PL0259
Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0259
R;Shlomchik, M.; Mascellli, M.; Shan, H.; Radic, M.2.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171,.265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0259
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 50 ATSSLDS 56

RESULT 4
KVMSM4
Ig kappa chain precursor V region (MOPC 41) - mouse
N;Contains: Ig kappa chain precursor V region VK41
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999
C;Accession: A93211; B93211; A93815; A94239; A01922; A01923
R;Seidman, J.G.; Max, E.E.; Leder, P.
Nature 280, 370-375, 1979
A;Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu
A;Reference number: A93211; MUID:79221900; PMID:111146
A;Accession: A93211
A;Molecule type: DNA
A;Residues: 1-130 <PC41>
A;Accession: B93211
A;Molecule type: DNA
A;Residues: 1-117 <VK41>
A;Cross-references: GB:V00804; GB:J00566; NID:g52127; PIDN:CAA24186.1; PID:g575660
A;Note: the sequences were determined from the differentiated gene MOPC 41 and the germ
R;Burststein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Accession: A93815
A;Molecule type: protein
A;Residues: 1-33 <BUR>
A;Note: Met-3 is apparently used as an alternative initiator in 25% of the chains

R;Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A;Title: Mechanism of antibody synthesis: size differences between mouse kappa chains
A;Reference number: A94239; MUID:67056897; PMID:4162931
A;Accession: A94239
A;Molecule type: protein
A;Residues: 23-49,'B',51-53,'LSB',57-58,'22',61-62,'BZ',65-76,'B',78-108,110-130 <GRA
A;Experimental source: Bence Jones protein MOPC 41
C;Genetics:
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: alternative initiators; heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status experimental <SIG1>
F;3-22/Domain: signal sequence #status experimental <SIG2>
F;23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 72 ATSSLDS 78

RESULT 5
E97737
hypothetical protein RC0301 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 19-Jul-2002
C;Accession: E97737
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: E97737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL02839.1; PID:g15619360; GSPDB:GN00173
C;Genetics:
A;Gene: RC0301
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 62 ATSSLDS 68

RESULT 6
AI3469
ABC transporter ATP-binding protein BMEI1743 [imported] - Brucella melitensis (strain
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3469
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-320 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52924.1; PID:g17983771; GSPDB:GN00190

A;Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1743
A:Map position: 1

Query Match 100.0%; Score 31; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||

Db 235 ATSSLDS 241

RESULT 7
F71732
ABC transporter ATP-binding protein (abct3) RP214 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C:Accession: F71732
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: F71732
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-548 <AND>
A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14677.1; PID:e134252
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: abct3; RP214
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C:Keywords: ATP
F:323-517/Domain: ATP-binding cassette homology <ABC>

Query Match 100.0%; Score 31; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||

Db 470 ATSSLDS 476

RESULT 8
S63137
hypothetical protein YNL182c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N1636
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
C:Accession: S63137
R:Obermaier, B.; Piravandi, E.; Rinke, M.; Domdey, H.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63122
A:Accession: S63137
A:Molecule type: DNA
A:Residues: 1-555 <OBE>
A:Cross-references: EMBL:Z71458; NID:gl302165; PID:e239555; PID:gl302166; GSPDB:GN00014;
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YNL182C
A:Cross-references: SGD:S0005126
A:Map position: 14L

Query Match 100.0%; Score 31; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||

Db 506 ATSSLDS 512

RESULT 9
D70031
ABC transporter (ATP-binding protein) homolog yvcc - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C:Accession: D70031
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70031
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-589 <KUN>
A:Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15487.1; PID:g26359
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvcc
C:Superfamily: Escherichia coli ABC transporter mdlA; ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop
F:357-552/Domain: ATP-binding cassette homology <ABC>
F:374-381/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||

Db 505 ATSSLDS 511

RESULT 10
F97735
hypothetical protein abct3 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C:Accession: F97735
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: F97735
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-589 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAL02824.1; PID:gl5619343; GSPDB:GN00173
C:Genetics:
A:Gene: abct3
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||

Db 511 ATSSLDS 517

RESULT 11
AD3138
hypoetical protein exsA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 17-May-2002
C;Accession: AD3138
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AD3138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-600 <KUR>
A;Cross-references: GB:AE008689; PIDN: AAL45522.1; PID: g17743233; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: exsA
A;Map position: linear chromosome
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 517 ATSSLDS 523

RESULT 12
H98149
ATP-binding transport protein exsA [imported] - Agrobacterium tumefaciens (strain C58, C
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: H98149
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: H98149
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-600 <KUR>
A;Cross-references: GB:AE007870; PIDN: AAK88722.1; PID: g15158459; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_309
A;Map position: linear chromosome

Query Match 100.0%; Score 31; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 517 ATSSLDS 523

RESULT 13
S60182
ATP-binding transport protein exsA - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 02-Feb-2001
C;Accession: S60182
R;Becker, A.; Kuester, H.; Niehaus, K.; Puehler, A.
Mol. Gen. Genet. 249, 487-497, 1995
A;Title: Extension of the Rhizobium meliloti succinoglycan biosynthesis gene cluster: id
regulator of succinoglycan biosynthesis.

A;Reference number: S60181; MUID:96133689; PMID:8544814
A;Accession: S60182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-604 <BEC>
A;Cross-references: EMBL:250189; NID:g1143532; PIDN:CAA90568.1; PID:el91488; PID:g114
A;Note: it is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the init
C;Genetics:
A;Gene: exsA
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C;Keywords: ATP; nucleotide binding; P-loop
F;371-565/Domain: ATP-binding cassette homology <ABC>
F;388-395/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 31; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 518 ATSSLDS 524

RESULT 14
H95974
msbA-like saccharide exporting ABC transporter protein, consisting of ATP-binding and
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: H95974
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H95974
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-604 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49464.1; PID:g15140950; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Genetics:
A;Gene: exsA; SMB20941
A;Genome: plasmid

Query Match 100.0%; Score 31; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||
Db 518 ATSSLDS 524

RESULT 15
T18376
multidrug resistance protein 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18376
R;Rubio, J.P.; Cowman, A.F.
Exp. Parasitol. 79, 137-147, 1994
A;Title: Plasmodium falciparum: the pfmdr2 protein is not overexpressed in chloroquin
A;Reference number: Z18924; MUID:94333528; PMID:7914495
A;Accession: T18376
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-1025 <RUB>
A;Cross-references: EMBL:U04640; NID:g439853; PID:g439854; PIDN:AAA21513.1
C;Genetics:
A;Gene: mdr2

Query Match 100.0%; Score 31; DB 2; Length 1025;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
| | | | | | |
Db 851 ATSSLDS 857

Search completed: March 10, 2003, 17:01:23
Job time : 8.60345 secs

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 9.77586 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	47	100.0	98	2 PH1062	Ig light chain V r
2	47	100.0	101	2 C28840	Ig kappa chain V r
3	47	100.0	101	2 B28840	Ig kappa chain V r
4	43	91.5	92	2 D28840	Ig kappa chain V r
5	42	89.4	88	2 PL0261	Ig kappa chain V r
6	42	89.4	106	2 PL0260	Ig kappa chain V r
7	42	89.4	130	1 KVMSM4	Ig kappa chain pre
8	40	85.1	321	1 S57530	carboxyl esterase
9	39	83.0	91	2 S67940	Ig kappa chain V r
10	39	83.0	92	2 S37513	Ig kappa chain V r
11	39	83.0	106	2 PL0259	Ig kappa chain V r
12	39	83.0	109	2 A30608	Ig kappa chain V r
13	39	83.0	109	2 H30601	Ig kappa chain V-I
14	37	78.7	128	1 K3HU41	Ig kappa chain pre
15	36	76.6	106	2 PL0262	Ig kappa chain V r
16	36	76.6	282	1 G64120	phot protein - Hae
17	36	76.6	947	2 G86557	polymorphic membra
18	36	76.6	947	2 D72067	polymorphic membra
19	35	74.5	92	2 S37524	Ig kappa chain V r
20	35	74.5	108	1 K3HUB6	Ig kappa chain V-I
21	35	74.5	109	2 G30607	Ig kappa chain V-I
22	35	74.5	117	1 KVMS3B	Ig kappa chain pre
23	35	74.5	536	2 A99283	hypothetical prote
24	35	74.5	619	2 B97475	hypothetical prote
25	35	74.5	619	2 AF2693	conserved hypothet
26	35	74.5	761	2 T33816	hypothetical prote
27	35	74.5	1290	2 A56493	leucocyte common a
28	35	74.5	1897	1 TDHULK	leukocyte antigen-
29	35	74.5	1898	2 S46216	leukocyte antigen-

30	34	72.3	103	2 S13703	Ig kappa chain V r
31	34	72.3	104	2 S13700	Ig kappa chain V r
32	34	72.3	106	2 A49138	IgA kappa rheumato
33	34	72.3	108	2 C30608	Ig kappa chain V-I
34	34	72.3	117	2 S42466	Ig kappa chain V r
35	34	72.3	129	1 K3HUHI	Ig kappa chain pre
36	34	72.3	131	2 C24356	hypothetical prote
37	34	72.3	131	2 S49388	gene Cx protein -
38	34	72.3	211	2 T47976	hypothetical prote
39	34	72.3	240	2 S06084	Ig kappa chain pre
40	34	72.3	287	2 C82593	ABC transporter ph
41	34	72.3	461	2 C64796	dcuC protein - Esc
42	34	72.3	461	2 D90711	c4-dicarboxylate a
43	34	72.3	461	2 H85561	transport of dicar
44	34	72.3	461	2 AF0579	C4-dicarboxylate a
45	34	72.3	572	2 TL2496	hypothetical prote

ALIGNMENTS

RESULT 1
PH1062
Ig light chain V region (clone 202.105) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1062
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1062
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 89 LQYASSPYT 97

RESULT 2
C28840
Ig kappa chain V region (HP22) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jan-2000
C;Accession: C28840; J25114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A;Title: The idiotypic network and the internal image: possible regulation of a germ-
A;Reference number: A91028; MUID:86136012; PMID:3937730
A;Accession: C28840
A;Molecule type: mRNA
A;Residues: 1-101 <OLL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;10-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 47; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 83 LQYASSPYT 91

A:Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
R:Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A:Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.
A:Reference number: A94239; MUID:67056897; PMID:4162931
A:Accession: A94239
A:Molecule type: protein
A:Residues: 23-49, 'B', 51-53, 'LSB', 57-58, 'ZZ', 61-62, 'BZ', 65-76, 'B', 78-108, 110-130 <GRA>
A:Experimental source: Bence Jones protein MOPC 41
C:Genetics:
A:Introns: 19/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: alternative initiators; heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status experimental <SIG1>
F:3-22/Domain: signal sequence #status experimental <SIG2>
F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F:38-112/Domain: immunoglobulin homology <IMM>
F:45-110/Disulfide bonds: #status predicted

Query Match 89.4%; Score 42; DB 1; Length 130;
Best Local Similarity 88.9%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||:|||||
Db 111 LQYASSPWT 119

RESULT 8
S57530
carboxyl esterase - Acinetobacter calcoaceticus
C:Species: Acinetobacter calcoaceticus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S57530
R:Kok, R.G.; Bart, A.; Hellingwerf, K.J.
submitted to the EMBL Data Library, June 1995
A:Description: Characterization of the estBR operon of Acinetobacter calcoaceticus BD413
A:Reference number: S57529

A:Accession: S57530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-321 <KOK>
A:Cross-references: EMBL:X88895
C:Genetics:
A:Start codon: GTG
C:Superfamily: carboxyl esterase

Query Match 85.1%; Score 40; DB 1; Length 321;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
||:|||||
Db 14 LQFSSSPYT 22

RESULT 9
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C:Accession: S67940
R:Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A:Title: Cloning of a human autoimmune response: preparation and sequencing of a human alpha 1 chain.
A:Reference number: S67940; MUID:92314301; PMID:1617110

A:Accession: S67940
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <HEX>
A:Cross-references: EMBL:X73852

C:Superfamily: immunoglobulin V region; immunoglobulin homology
Query Match 83.0%; Score 39; DB 2; Length 91;
Best Local Similarity 87.5%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|||:|||||
Db 72 QYGSSPYT 79

RESULT 10
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37513
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood.
A:Reference number: S37501
A:Accession: S37513
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26598; NID:9405668; PIDN:CAA81352.1; PID:9405669
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin.

Query Match 83.0%; Score 39; DB 2; Length 92;
Best Local Similarity 87.5%; Pred. No. 0.82;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|||:|||||
Db 74 QYGSSPYT 81

RESULT 11
PL0259
Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0259
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.2.; Pisetsky, D.; Marshak-Rothstein, J.
Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation.
A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0259
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 83.0%; Score 39; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 0.95;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||:|||||
Db 89 LQYATSPWT 97

RESULT 12
A30608

Ig kappa chain V-III region (Son) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: A30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: A30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 39; DB 2; Length 109;
Best Local Similarity 87.5%; Pred. No. 0.98;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|||
Db 91 QYGSSPYT 98

RESULT 13
H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: H30601; E30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: H30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON1>
A;Accession: E30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 39; DB 2; Length 109;
Best Local Similarity 87.5%; Pred. No. 0.98;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|||
Db 91 QYGSSPYT 98

RESULT 14
K3H041
Ig kappa chain precursor V-III region (IARC/BL41) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C;Accession: A01899
R;Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A;Reference number: A93588; MUID:86041852; PMID:2997711
A;Accession: A01899
A;Molecule type: DNA
A;Residues: 1-128 <KLO>
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266

A;Map position: 2p12-2p11
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-128/Product: Ig kappa chain V-III region (IARC/BL41) #status predicted <MAT>
F;21-43/Region: framework 1
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;55-69/Region: framework 2
F;70-76/Region: complementarity-determining 2
F;77-108/Region: framework 3
F;109-117/Region: complementarity-determining 3
F;118-128/Region: framework 4
F;43-108/Disulfide bonds: #status predicted

Query Match 78.7%; Score 37; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 3;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
|||
Db 110 QYSTSPYT 117

RESULT 15
PL0262
Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0262
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.2.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0262
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match 76.6%; Score 36; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||
Db 89 LQYASYPWT 97

Search completed: March 10, 2003, 17:01:24
Job time : 10.7759 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 9.82759 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	82.8	117	2 US-08-814-806-4	Sequence 4, Appli
2	48	82.8	142	2 US-08-678-194-8	Sequence 8, Appli
3	48	82.8	142	4 US-08-890-011-8	Sequence 8, Appli
4	48	82.8	142	4 US-09-262-724-8	Sequence 8, Appli
5	47	81.0	123	1 US-08-497-312-15	Sequence 15, Appl
6	47	81.0	123	1 US-08-497-312-17	Sequence 17, Appl
7	47	81.0	123	2 US-08-560-558E-28	Sequence 28, Appl
8	46	79.3	110	4 US-09-214-095D-86	Sequence 86, Appl
9	46	79.3	116	2 US-08-672-345C-105	Sequence 105, App
10	46	79.3	116	2 US-08-672-345C-106	Sequence 106, App
11	46	79.3	116	4 US-09-214-095D-90	Sequence 90, Appl
12	45	77.6	115	2 US-08-672-345C-18	Sequence 18, Appl
13	45	77.6	115	2 US-08-672-345C-108	Sequence 108, App
14	45	77.6	115	4 US-09-214-095D-18	Sequence 18, Appl
15	45	77.6	115	4 US-09-214-095D-98	Sequence 98, Appl
16	45	77.6	118	1 US-08-477-877B-93	Sequence 93, Appl
17	45	77.6	118	2 US-08-472-281A-93	Sequence 93, Appl
18	45	77.6	118	2 US-08-477-989B-93	Sequence 93, Appl
19	45	77.6	137	1 US-08-477-877B-96	Sequence 96, Appl
20	45	77.6	137	2 US-08-472-281A-96	Sequence 96, Appl
21	45	77.6	137	2 US-08-477-989B-96	Sequence 96, Appl
22	45	77.6	138	3 US-08-603-024-2	Sequence 2, Appli
23	45	77.6	139	1 US-08-253-877C-8	Sequence 8, Appli
24	45	77.6	139	1 US-08-253-877C-19	Sequence 19, Appl
25	45	77.6	139	2 US-08-452-164A-8	Sequence 8, Appli
26	45	77.6	139	2 US-08-452-164A-19	Sequence 19, Appl
27	45	77.6	139	3 US-08-603-024-18	Sequence 18, Appl

28	44	75.9	116	2	US-08-561-521-41	Sequence 41, Appl
29	44	75.9	116	5	PCT-US95-01219-41	Sequence 41, Appl
30	44	75.9	135	1	US-08-137-117D-27	Sequence 27, Appl
31	44	75.9	135	1	US-08-137-117D-100	Sequence 100, App
32	44	75.9	135	1	US-08-137-117D-102	Sequence 102, App
33	44	75.9	135	1	US-08-137-117D-112	Sequence 112, App
34	44	75.9	135	2	US-08-436-717-27	Sequence 27, Appl
35	44	75.9	135	2	US-08-436-717-100	Sequence 100, App
36	44	75.9	135	2	US-08-436-717-102	Sequence 102, App
37	44	75.9	135	2	US-08-436-717-112	Sequence 112, App
38	43	74.1	116	2	US-08-737-560A-7	Sequence 7, Appli
39	43	74.1	124	2	US-08-657-012-16	Sequence 16, Appl
40	43	74.1	124	2	US-08-657-012-17	Sequence 17, Appl
41	43	74.1	124	2	US-08-657-012-18	Sequence 18, Appl
42	43	74.1	124	2	US-08-657-012-19	Sequence 19, Appl
43	43	74.1	124	2	US-08-657-012-23	Sequence 23, Appl
44	43	74.1	124	3	US-09-013-872-16	Sequence 16, Appl
45	43	74.1	124	3	US-09-013-872-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-814-806-4
; Sequence 4, Application US/08814806
; Patent No. 5986065
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; APPLICANT: Jiao, Jin-an
; APPLICANT: Esperanza, Nieves
; APPLICANT: Lawrence, Luepschen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,806
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

US-08-814-806-4

Query Match 82.8%; Score 48; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.49;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|||||||:
Db 26 GYSFTDYNVY 35

RESULT 2

US-08-678-194-8
; Sequence 8, Application US/08678194
; Patent No. 5922845

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; TITLE OF INVENTION: Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"} Receptor Antibodi

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194

; FILING DATE: July 11, 1996

; PRIOR APPLICATION DATA: No. 5922845e

; APPLICATION NUMBER: US

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Beth A. Arnold

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MXI-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 142 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-678-194-8

Query Match 82.8%; Score 48; DB 2; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|||||||:
Db 45 GYSFTDYIIF 54

RESULT 3

US-08-890-011-8

; Sequence 8, Application US/08890011

; Patent No. 6193966

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; APPLICANT: Graziano, Robert

; APPLICANT: Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; TITLE OF INVENTION: Comprised of Anti-Fc
; TITLE OF INVENTION: {SYMBOL 97 \f "Symbol"} Receptor Antibodies
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/890,011

; FILING DATE: July 9, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/678,194

; FILING DATE: July 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Jane E. Remillard

; REGISTRATION NUMBER: 38,872

; REFERENCE/DOCKET NUMBER: MXI-064CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 142 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-890-011-8

Query Match 82.8%; Score 48; DB 4; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|||||||:
Db 45 GYSFTDYIIF 54

RESULT 4

US-09-262-724-8

; Sequence 8, Application US/09262724

; Patent No. 6303755

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; APPLICANT: Graziano, Robert

; APPLICANT: Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; TITLE OF INVENTION: Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"} Receptor Antibodies

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,724

; FILING DATE: 04-Mar-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194
; FILING DATE: July 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Beth A. Arnold
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-262-724-8

Query Match 82.8%; Score 48; DB 4; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 45 GYSFTDYIIF 54

RESULT 5
US-08-497-312-15
; Sequence 15, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 1PM04UT
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-497-312-15

Query Match 81.0%; Score 47; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 26 GYTFTNYIY 35

RESULT 6
US-08-497-312-17
; Sequence 17, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 1PM04UT
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-497-312-17

Query Match 81.0%; Score 47; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 26 GYTFTNYIY 35

RESULT 7
US-08-560-558E-28
; Sequence 28, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Humanized and chimeric monoclonal
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
; TITLE OF INVENTION: EGF-R); diagnostic and therapeutic use.

;
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
; STREET: P.O. Box 2250
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: United States of America
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS95
; SOFTWARE: Wordperfect 5.1/5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,558E
; FILING DATE: No. 5891996ember 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33,041
; REFERENCE/DOCKET NUMBER: 2720US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 532-1922
; TELEFAX: (801) 531-9168
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-560-558E-28

Query Match 81.0%; Score 47; DB 2; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
||:|:|:|:|
Db 26 GYFTNYYIY 35

RESULT 8
US-09-214-095D-86
; Sequence 86, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Murine
; US-09-214-095D-86

Query Match 79.3%; Score 46; DB 4; Length 110;
Best Local Similarity 80.0%; Pred. No. 0.97;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
|||||:|
Db 20 GYSFTDYNMY 29

RESULT 9
US-08-672-345C-105
; Sequence 105, Application US/08672345C
; Patent No. 5948658

;
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-672-345C-105

Query Match 79.3%; Score 46; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
|||||:|
Db 26 GYSFTDYNMY 35

RESULT 10
US-08-672-345C-106
; Sequence 106, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-106

Query Match 79.3%; Score 46; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 GYSFTDYFIY 10
||| | | | | | : |
Db 26 GYSFTDYNMY 35

RESULT 11
US-09-214-095D-90
Sequence 90, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: 116
TYPE: PRT
ORGANISM: Murine
US-09-214-095D-90

Query Match 79.3%; Score 46; DB 4; Length 116;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 GYSFTDYFIY 10
||| | | | | | : |
Db 26 GYSFTDYNMY 35

RESULT 12
US-08-672-345C-18
Sequence 18, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-18

Query Match 77.6%; Score 45; DB 2; Length 115;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 GYSFTDYFIY 10
||| | | | | | : |
Db 25 GYTFTTYIY 34

RESULT 13
US-08-672-345C-108
Sequence 108, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-672-345C-108

Query Match 77.6%; Score 45; DB 2; Length 115;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 GYSFTDYFIY 10
||| | | | | | : |
Db 25 GYTFTTYIY 34

RESULT 14
US-09-214-095D-18
; Sequence 18, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-18

Query Match 77.6%; Score 45; DB 4; Length 115;
Best Local Similarity 70.0%; Pred. NO. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
||:||||:|
Db 25 GYFTTYIY 34

RESULT 15
US-09-214-095D-98
; Sequence 98, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-98

Query Match 77.6%; Score 45; DB 4; Length 115;
Best Local Similarity 70.0%; Pred. NO. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
||:||||:|
Db 25 GYFTTYIY 34

Search completed: March 10, 2003, 17:02:32
Job time : 10.8276 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 16.7069 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	74	76.3	237	2	US-08-468-252-5
2	74	76.3	237	3	US-08-668-706B-5
3	74	76.3	237	5	PCT-US95-10740-5
4	71	73.2	17	1	US-08-137-117D-144
5	71	73.2	17	2	US-08-436-717-144
6	71	73.2	108	2	US-08-888-366-6
7	71	73.2	116	2	US-08-561-521-41
8	71	73.2	116	5	PCT-US95-01219-41
9	71	73.2	135	1	US-08-137-117D-27
10	71	73.2	135	1	US-08-137-117D-100
11	71	73.2	135	1	US-08-137-117D-102
12	71	73.2	135	1	US-08-137-117D-112
13	71	73.2	135	2	US-08-436-717-27
14	71	73.2	135	2	US-08-436-717-100
15	71	73.2	135	2	US-08-436-717-102
16	71	73.2	135	2	US-08-436-717-112
17	70	72.2	119	1	US-07-634-278-64
18	70	72.2	119	1	US-07-634-278-65
19	70	72.2	119	1	US-07-634-278-89
20	70	72.2	119	1	US-08-477-728-64
21	70	72.2	119	1	US-08-477-728-65
22	70	72.2	119	1	US-08-477-728-89
23	70	72.2	119	1	US-08-474-040-64
24	70	72.2	119	1	US-08-474-040-65
25	70	72.2	119	1	US-08-474-040-89
26	70	72.2	119	1	US-08-487-200-64
27	70	72.2	119	1	US-08-487-200-65

28	70	72.2	119	1	US-08-487-200-89	Sequence 89, Appl
29	70	72.2	119	4	US-08-484-537-64	Sequence 64, Appl
30	70	72.2	119	4	US-08-484-537-65	Sequence 65, Appl
31	70	72.2	119	4	US-08-484-537-89	Sequence 89, Appl
32	70	72.2	138	1	US-07-634-278-85	Sequence 85, Appl
33	70	72.2	138	1	US-08-477-728-85	Sequence 85, Appl
34	70	72.2	138	1	US-08-474-040-85	Sequence 85, Appl
35	70	72.2	138	1	US-08-487-200-85	Sequence 85, Appl
36	70	72.2	138	4	US-08-484-537-85	Sequence 85, Appl
37	70	72.2	243	1	US-08-230-843-4	Sequence 4, Appli
38	70	72.2	243	2	US-08-636-936-4	Sequence 4, Appli
39	69	71.1	117	4	US-08-525-539A-76	Sequence 76, Appl
40	69	71.1	117	4	US-08-525-539A-78	Sequence 78, Appl
41	69	71.1	136	4	US-08-525-539A-47	Sequence 47, Appl
42	69	71.1	136	4	US-08-525-539A-63	Sequence 63, Appl
43	68	70.1	273	2	US-08-403-853-18	Sequence 18, Appl
44	67	69.1	115	2	US-08-672-345C-16	Sequence 16, Appl
45	67	69.1	115	4	US-09-214-095D-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-468-252-5
; Sequence 5, Application US/08468252
; Patent No. 5910486
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Deshane, Jessy
; APPLICANT: King, C. Richter
; TITLE OF INVENTION: Methods for Modulating Protein Function in
; TITLE OF INVENTION: Cells Using Intracellular Antibody Homologues
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,252
; FILING DATE: 06-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Geary, William C. III
; REGISTRATION NUMBER: 31,359
; REFERENCE/DOCKET NUMBER: UAG-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-252-5

Query Match 76.3%; Score 74; DB 2; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00012;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16

1:|||||:||||:

Db 171 INPYNGDTNYNQKFK 185

RESULT 2
US-08-668-706B-5
; Sequence 5, Application US/08668706B
; Patent No. 6028059
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Deshane, Jessy
; APPLICANT: King, C. Richter
; TITLE OF INVENTION: Methods for Modulating Protein Function in
; TITLE OF INVENTION: Cells Using Intracellular Antibody Homologues
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,706B
; FILING DATE: June 24, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Benjamin Aaron
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5874CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: No
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
US-08-668-706B-5
Query Match 76.3%; Score 74; DB 3; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00012;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFR 16
I:|||||:|||||
Db 171 INPYNGDTNYNQKFK 185
RESULT 3
PCT-US95-10740-5
; Sequence 5, Application PC/TUS9510740
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Deshane, Jessy
; APPLICANT: King, C. Richter
; TITLE OF INVENTION: Methods for Modulating Protein Function in Cells Using Intra
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10740
; FILING DATE: 06-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Geary, William C. III
; REGISTRATION NUMBER: 31,359
; REFERENCE/DOCKET NUMBER: UAG-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-10740-5
Query Match 76.3%; Score 74; DB 5; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00012;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFR 16
I:|||||:|||||
Db 171 INPYNGDTNYNQKFK 185
RESULT 4
US-08-137-117D-144
; Sequence 144, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.

; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-137-117D-144

Query Match 73.2%; Score 71; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.9e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 2 IDPFNGGTSYNQKFK 16

RESULT 5
US-08-436-717-144
; Sequence 144, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-436-717-144

Query Match 73.2%; Score 71; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.9e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 2 IDPFNGGTSYNQKFK 16

RESULT 6
US-08-888-366-6
; Sequence 6, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-366-6

Query Match 73.2%; Score 71; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.00015;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16

;
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-27

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|||:| | | | | | | |
Db 70 IDPFNGGTSYNQKFK 84

RESULT 10
US-08-137-117D-100
; Sequence 100, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258

;
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-100

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|||:| | | | | | | |
Db 70 IDPFNGGTSYNQKFK 84

RESULT 11
US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-137-117D-102

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|||:| | |||||:
Db 70 IDPFNGGTSYNQKFK 84

RESULT 12
US-08-137-117D-112
; Sequence 112, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-112

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|||:| | |||||:
Db 70 IDPFNGGTSYNQKFK 84

RESULT 13
US-08-436-717-27
; Sequence 27, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-27

Query Match 73.2%; Score 71; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|||:| | |||||:
Db 70 IDPFNGGTSYNQKFK 84

RESULT 14
US-08-436-717-100
; Sequence 100, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki

```

; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-717-100

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Query Match 73.2%; Score 71; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels

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Qy      2 IDPYNGDTSYNQKFR 16
        |||:| | | | | | |
Db     70 IDPENGGTSYNOKEK 84
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RESULT 15
US-08-436-717-102
; Sequence 102, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
;
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-436-717-102

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Query Match 73.2%; Score 71; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2 IDPYNGDTSYNQKER 16
      III:II IIIIIII:
Db     70 IDPFNGGTSYNQKEK 84
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Search completed: March 10, 2003, 17:02:32
Job time : 16.7069 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 3.93103 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					% Match		Query Length		DB ID		Description	
Result No.	Score	Match	Length	DB	ID							
1	21	100.0	6	4	US-09-170-769A-15						Sequence 15, Appl	
2	21	100.0	15	4	US-09-026-904-14						Sequence 14, Appl	
3	21	100.0	15	6	5248606-25						Patent No. 5248606	
4	21	100.0	18	2	US-09-017-205-22						Sequence 22, Appl	
5	21	100.0	18	2	US-09-017-205-23						Sequence 23, Appl	
6	21	100.0	24	1	US-08-434-198-1						Sequence 1, Appli	
7	21	100.0	24	1	US-08-434-198-4						Sequence 4, Appli	
8	21	100.0	25	3	US-08-904-446A-12						Sequence 12, Appl	
9	21	100.0	26	2	US-08-620-151-13						Sequence 13, Appl	
10	21	100.0	30	4	US-09-230-405-11						Sequence 11, Appl	
11	21	100.0	40	4	US-08-905-223-387						Sequence 387, App	
12	21	100.0	43	2	US-09-097-759-1						Sequence 1, Appli	
13	21	100.0	49	1	US-08-178-477B-6						Sequence 6, Appli	
14	21	100.0	66	1	US-08-450-360-10						Sequence 10, Appl	
15	21	100.0	87	2	US-08-461-990B-20						Sequence 20, Appl	
16	21	100.0	92	4	US-09-247-155-98						Sequence 98, Appl	
17	21	100.0	109	4	US-09-134-001C-3975						Sequence 3975, Ap	
18	21	100.0	113	6	5248606-47						Patent No. 5248606	
19	21	100.0	119	1	US-08-300-386A-65						Sequence 65, Appl	
20	21	100.0	119	3	US-08-931-645-65						Sequence 65, Appl	
21	21	100.0	119	5	PCT-US95-11235-65						Sequence 65, Appl	
22	21	100.0	136	3	US-09-187-049-6						Sequence 6, Appli	
23	21	100.0	136	4	US-09-222-938A-55						Sequence 55, Appl	
24	21	100.0	138	4	US-09-149-476-390						Sequence 390, App	
25	21	100.0	140	2	US-08-449-287-4						Sequence 4, Appli	
26	21	100.0	146	2	US-08-449-287-10						Sequence 10, Appl	
27	21	100.0	146	2	US-08-449-287-12						Sequence 12, Appl	

28	21	100.0	149	2	US-08-606-143-24	Sequence 24, Appl
29	21	100.0	150	2	US-08-606-143-26	Sequence 26, Appl
30	21	100.0	150	2	US-08-606-143-29	Sequence 29, Appl
31	21	100.0	151	2	US-08-606-143-19	Sequence 19, Appl
32	21	100.0	152	2	US-08-606-143-4	Sequence 4, Appli
33	21	100.0	152	2	US-08-606-143-5	Sequence 5, Appli
34	21	100.0	152	2	US-08-606-143-6	Sequence 6, Appli
35	21	100.0	152	2	US-08-606-143-7	Sequence 7, Appli
36	21	100.0	152	2	US-08-606-143-9	Sequence 9, Appli
37	21	100.0	152	2	US-08-606-143-10	Sequence 10, Appl
38	21	100.0	152	2	US-08-606-143-12	Sequence 12, Appl
39	21	100.0	152	2	US-08-606-143-13	Sequence 13, Appl
40	21	100.0	152	2	US-08-606-143-15	Sequence 15, Appl
41	21	100.0	152	2	US-08-606-143-16	Sequence 16, Appl
42	21	100.0	152	2	US-08-606-143-18	Sequence 18, Appl
43	21	100.0	152	2	US-08-606-143-20	Sequence 20, Appl
44	21	100.0	152	2	US-08-606-143-21	Sequence 21, Appl
45	21	100.0	152	2	US-08-606-143-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-170-769A-15

; Sequence 15, Application US/09170769A

; Patent No. 6444206

; GENERAL INFORMATION:

; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE

; APPLICANT: LETURCO, Didier

; APPLICANT: MORIATRY, Ann

; APPLICANT: ULEVITCH, Richard

; APPLICANT: TOBIAS, Peter

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACT

; FILE REFERENCE: SCRIP1140-3

; CURRENT APPLICATION NUMBER: US/09/170,769A

; CURRENT FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: US 08/070,160

; PRIOR FILING DATE: 1993-05-28

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Murine

US-09-170-769A-15

Query Match 100.0%; Score 21; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
| | | |
Db 1 GLRF 4

RESULT 2

US-09-026-904-14

; Sequence 14, Application US/09026904

; Patent No. 6245502

; GENERAL INFORMATION:

; APPLICANT: Emi, B.

; TITLE OF INVENTION: TARGET SYSTEM

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,904
FILING DATE: Concurrently herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gerald J. Flintoft
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-026-904-14

Query Match 100.0%; Score 21; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
|
Db 1 GLRF 4

RESULT 3
5248606-25
PATENT NO. 5248606
APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN, ALICE E.R.
TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
NUMBER OF SEQUENCES: 49
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/535,636
FILING DATE: 11-JUN-1990
SEQ ID NO: 25:
LENGTH: 15
5248606-25

Query Match 100.0%; Score 21; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
|
Db 8 GLRF 11

RESULT 4
US-09-017-205-22
Sequence 22, Application US/09017205
Patent No. 5965357
GENERAL INFORMATION:
APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-436
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide from HSV-2 glycoprotein G
FRAGMENT TYPE: internal
US-09-017-205-22

Query Match 100.0%; Score 21; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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|
|
|
Db 15 GLRF 18

RESULT 5
US-09-017-205-23
Sequence 23, Application US/09017205
Patent No. 5965357
GENERAL INFORMATION:
APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-436
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide from HSV-2 glycoprotein G
FRAGMENT TYPE: internal
US-09-017-205-23

Query Match 100.0%; Score 21; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 5 GLRF 8

RESULT 6

US-08-434-198-1
; Sequence 1, Application US/08434198
; Patent No. 5688911
; GENERAL INFORMATION:
; APPLICANT: Schneider, et al.
; TITLE OF INVENTION: TRK Neurotrophin Binding Motifs
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,198
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Kempler PhD., Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-434-198-1

Query Match 100.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 6 GLRF 9

RESULT 7

US-08-434-198-4
; Sequence 4, Application US/08434198
; Patent No. 5688911
; GENERAL INFORMATION:
; APPLICANT: Schneider, et al.
; TITLE OF INVENTION: TRK Neurotrophin Binding Motifs
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

ZIP: 10591-6707
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,198
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Kempler PhD., Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-434-198-4

Query Match 100.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 6 GLRF 9

RESULT 8

US-08-904-446A-12
; Sequence 12, Application US/08904446A
; Patent No. 6029114
; GENERAL INFORMATION:
; APPLICANT: Shamovsky, Igor L.
; APPLICANT: Ross, Gregory M.
; APPLICANT: Riopelle, Richard J.
; APPLICANT: Weaver, Donald F.
; TITLE OF INVENTION: Molecular Modelling of Neurotrophin-Receptor
; TITLE OF INVENTION: Binding
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowell & Dowell, P.C.
; STREET: 1215 Jefferson Davis Highway, Suite 309
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,446A
; FILING DATE: 31-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9616105.4
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: RALPH A. DOWELL
; REGISTRATION NUMBER: 26868
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-2555
; TELEFAX: (703) 415-2559
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..25
; OTHER INFORMATION: /note= "Second leucine rich motif
; OTHER INFORMATION:
US-08-904-446A-12

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 10 GLRF 13

RESULT 9
US-08-620-151-13
; Sequence 13, Application US/08620151
; Patent No. 5928955
; GENERAL INFORMATION:
; APPLICANT: Imperiali, Barbara
; APPLICANT: Walkup, Grant K.
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
; TITLE OF INVENTION: DIVALENT ZINC
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; STREET: Plaza Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60611-5599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,151
; FILING DATE: 22-MAR-1996
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: Shannon, Karen L.
; REGISTRATION NUMBER: 36,675
; REFERENCE/DOCKET NUMBER: 8597/6
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-620-151-13

Query Match 100.0%; Score 21; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 8 GLRF 11

RESULT 10
US-09-230-405-11
; Sequence 11, Application US/09230405
; Patent No. 6337074
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-VIRAL AGENT
; FILE REFERENCE: P17970C
; CURRENT APPLICATION NUMBER: US/09/230,405
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide derived
; OTHER INFORMATION: from herpes simplex virus
US-09-230-405-11

Query Match 100.0%; Score 21; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 22 GLRF 25

RESULT 11
US-08-905-223-387
; Sequence 387, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 387:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:

;
; NAME/KEY: sig_peptide
; LOCATION: -36...-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 3.8
; OTHER INFORMATION: seq GTDLSFLPPPC/CP
US-08-905-223-387

Query Match 100.0%; Score 21; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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|
|
Db 6 GLRF 9

RESULT 12

US-09-097-759-1
; Sequence 1, Application US/09097759A
; Patent No. 5972663

; GENERAL INFORMATION:
; APPLICANT: Winterhalter Mr., Christopher

; APPLICANT: Leinfelder Mr., Walfred
; TITLE OF INVENTION: Microorganisms and Processes for the Fermentative

; TITLE OF INVENTION: Preparation of L-cysteine,
; TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives

; FILE REFERENCE: Winterhalter
; CURRENT APPLICATION NUMBER: US/09/097,759A

; CURRENT FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: DE 197 26 083

; EARLIER FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

; LENGTH: 43
; TYPE: PRT

; ORGANISM: Escherichia coli
US-09-097-759-1

Query Match 100.0%; Score 21; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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|
|
|
Db 37 GLRF 40

RESULT 13

US-08-178-477B-6
; Sequence 6, Application US/08178477B
; Patent No. 5756343

; GENERAL INFORMATION:
; APPLICANT: WU, CARL; CLOS, JOACHIM;

; APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN, SRIDHAR
; TITLE OF INVENTION: CELL STRESS

; TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE
; CITY: NEW YORK

; STATE: NEW YORK
; COUNTRY: USA

; ZIP: 10154
; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,477B

; FILING DATE: 07-JAN-1994

;
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/617,910
; FILING DATE: 26-NOV-1990
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4103US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-178-477B-6

Query Match 100.0%; Score 21; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
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|
Db 25 GLRF 28

RESULT 14

US-08-450-360-10
; Sequence 10, Application US/08450360
; Patent No. 5656457

; GENERAL INFORMATION:
; APPLICANT: Parkes, Deborah Lynn
; APPLICANT: Coates, Stephen Ralph

; TITLE OF INVENTION: Herpes Simplex Virus Type 2-Glycoprotein G
; TITLE OF INVENTION: Proteins and Polypeptides

; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder

; STREET: 6 Mariposa Court
; CITY: Tiburon

; STATE: California
; COUNTRY: USA

; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,360
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/129,021
; FILING DATE: 29-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0012.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727

; GENERAL INFORMATION:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-450-360-10

Query Match 100.0%; Score 21; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 48 GLRF 51

RESULT 15
US-08-461-990B-20
; Sequence 20, Application US/08461990B
; Patent No. 5851810
; GENERAL INFORMATION:
; APPLICANT: JOHN S. BLANCHARD
; TITLE OF INVENTION: NUCLEIC ACID ENCODING RHODOCOCCUS
; TITLE OF INVENTION: PHENYLALANINE DEHYDROGENASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,990B
; FILING DATE: JUNE 5, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG J. ARNOLD
; REGISTRATION NUMBER: 34,287
; REFERENCE/DOCKET NUMBER: 96700/370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PROTEIN
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: C. SYMBIOSUM
; INDIVIDUAL ISOLATE: GLUTAMATE DEHYDROGENASE
US-08-461-990B-20

Query Match 100.0%; Score 21; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 13 GLRF 16

Search completed: March 10, 2003, 17:02:33
Job time : 4.93103 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 8.10345 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	58	100.0	113	10 US-09-924-099-2	Sequence 2, Appli
3	58	100.0	237	10 US-09-924-099-9	Sequence 9, Appli
4	58	100.0	243	10 US-09-924-099-10	Sequence 10, Appli
5	48	82.8	117	9 US-09-293-854-4	Sequence 4, Appli
6	48	82.8	142	10 US-09-772-120-8	Sequence 8, Appli
7	47	81.0	123	10 US-09-217-268B-28	Sequence 28, Appli
8	47	81.0	123	10 US-09-217-268B-36	Sequence 36, Appli
9	44	75.9	98	9 US-10-194-975-11	Sequence 11, Appli
10	42	72.4	111	9 US-10-032-482-5	Sequence 5, Appli
11	42	72.4	125	9 US-09-929-665-20	Sequence 20, Appli
12	42	72.4	125	9 US-09-929-546-20	Sequence 20, Appli
13	42	72.4	249	1 US-08-779-457-48	Sequence 48, Appli
14	41	70.7	98	10 US-09-840-459-41	Sequence 41, Appli
15	41	70.7	118	9 US-09-144-886-63	Sequence 63, Appli
16	41	70.7	132	9 US-09-982-107-14	Sequence 14, Appli
17	41	70.7	669	9 US-09-807-721-2	Sequence 2, Appli
18	40	69.0	98	9 US-10-194-975-45	Sequence 45, Appli
19	40	69.0	98	10 US-09-850-165-89	Sequence 89, Appli

20	69.0	98	12	US-10-025-687-16	Sequence 16, Appli
21	69.0	120	12	US-10-025-687-6	Sequence 6, Appli
22	69.0	135	9	US-09-249-011A-2	Sequence 2, Appli
23	69.0	135	9	US-09-249-011A-6	Sequence 6, Appli
24	69.0	255	10	US-09-888-721-34	Sequence 34, Appli
25	69.0	262	9	US-09-956-086-4	Sequence 4, Appli
26	69.0	262	9	US-09-956-087-4	Sequence 4, Appli
27	69.0	269	10	US-09-888-721-36	Sequence 36, Appli
28	69.0	282	9	US-09-985-442-7	Sequence 7, Appli
29	69.0	282	10	US-09-888-721-38	Sequence 38, Appli
30	69.0	282	10	US-09-983-580-7	Sequence 7, Appli
31	69.0	287	10	US-09-888-721-40	Sequence 40, Appli
32	69.0	291	10	US-09-888-721-44	Sequence 44, Appli
33	69.0	296	10	US-09-888-721-42	Sequence 42, Appli
34	69.0	461	9	US-09-249-011A-24	Sequence 24, Appli
35	69.0	672	9	US-09-900-766-1	Sequence 1, Appli
36	67.2	118	10	US-09-905-243-70	Sequence 70, Appli
37	67.2	119	10	US-09-850-165-54	Sequence 54, Appli
38	67.2	128	10	US-09-850-165-52	Sequence 52, Appli
39	67.2	239	10	US-09-808-037-6	Sequence 6, Appli
40	65.5	96	10	US-09-905-243-15	Sequence 15, Appli
41	65.5	98	9	US-10-194-975-7	Sequence 7, Appli
42	65.5	100	10	US-09-840-459-37	Sequence 37, Appli
43	65.5	101	10	US-09-840-459-42	Sequence 42, Appli
44	65.5	101	10	US-09-840-459-46	Sequence 46, Appli
45	65.5	106	9	US-10-032-482-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-924-099-6
; Sequence 6, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-6

Query Match 100.0%; Score 58; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|||||
Db 1 GYSFTDYFIY 10

RESULT 2
US-09-924-099-2
; Sequence 2, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori


```

; APPLICANT:  TANIMOTO, Tadao
; APPLICANT:  KURIMOTO, Masashi
; TITLE OF INVENTION:  PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:  US/09/924,099
; CURRENT FILING DATE:  2001-08-08
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  09/338,511
; PRIOR FILING DATE:  EARLIER FILING DATE:  1999-06-23
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  JP 289,044/98
; PRIOR FILING DATE:  EARLIER FILING DATE:  1998-10-12
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  JP 365,023/98
; PRIOR FILING DATE:  EARLIER FILING DATE:  1998-12-22
; NUMBER OF SEQ ID NOS:  33
; SEQ ID NO 2
; LENGTH:  113
; TYPE:  PRT
; ORGANISM:  Mus musculus
US-09-924-099-2

Query Match      100.0%; Score 58; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
      |||||
Db      26 GYSFTDYFIY 35

RESULT 3
US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT:  NISHIDA, Yoshihiro
; APPLICANT:  OKURA, Takanori
; APPLICANT:  TANIMOTO, Tadao
; APPLICANT:  KURIMOTO, Masashi
; TITLE OF INVENTION:  PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:  US/09/924,099
; CURRENT FILING DATE:  2001-08-08
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  09/338,511
; PRIOR FILING DATE:  EARLIER FILING DATE:  1999-06-23
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  JP 289,044/98
; PRIOR FILING DATE:  EARLIER FILING DATE:  1998-10-12
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  JP 365,023/98
; PRIOR FILING DATE:  EARLIER FILING DATE:  1998-12-22
; NUMBER OF SEQ ID NOS:  33
; SEQ ID NO 9
; LENGTH:  237
; TYPE:  PRT
; ORGANISM:  Artificial Sequence
; FEATURE:
; OTHER INFORMATION:  Artificially produced peptide in the form of a single
; OTHER INFORMATION:  chain
; OTHER INFORMATION:  variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match      100.0%; Score 58; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
      |||||
Db      26 GYSFTDYFIY 35

RESULT 4
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT:  NISHIDA, Yoshihiro
```

```

; APPLICANT:  OKURA, Takanori
; APPLICANT:  TANIMOTO, Tadao
; APPLICANT:  KURIMOTO, Masashi
; TITLE OF INVENTION:  PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:  US/09/924,099
; CURRENT FILING DATE:  2001-08-08
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  09/338,511
; PRIOR FILING DATE:  EARLIER FILING DATE:  1999-06-23
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  JP 289,044/98
; PRIOR FILING DATE:  EARLIER FILING DATE:  1998-10-12
; PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  JP 365,023/98
; PRIOR FILING DATE:  EARLIER FILING DATE:  1998-12-22
; NUMBER OF SEQ ID NOS:  33
; SEQ ID NO 10
; LENGTH:  243
; TYPE:  PRT
; ORGANISM:  Artificial Sequence
; FEATURE:
; OTHER INFORMATION:  Artificially produced peptide in the form of a single
; OTHER INFORMATION:  chain
; OTHER INFORMATION:  variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match      100.0%; Score 58; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
      |||||
Db      26 GYSFTDYFIY 35

RESULT 5
US-09-293-854-4
; Sequence 4, Application US/09293854
; Patent No. US20020168357A1
; GENERAL INFORMATION:
; APPLICANT:  Wong, Hing C.
;             Jiao, Jin-an
;             Esperanza, Nieves
;             Lawrence, Luepschen
; TITLE OF INVENTION:  ANTIBODIES FOR INHIBITING BLOOD
;                     COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES:  26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Dike, Bronstein, Roberts & Cushman, LLP
; STREET:  130 Water Street
; CITY:  Boston
; STATE:  MA
; COUNTRY:  USA
; ZIP:  02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Diskette
; COMPUTER:  IBM Compatible
; OPERATING SYSTEM:  DOS
; SOFTWARE:  FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/09/293,854
; FILING DATE:  16-Apr-1999
; CLASSIFICATION:  <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  08/814,806
; FILING DATE:  <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME:  Corless, Peter F
; REGISTRATION NUMBER:  33,860
; REFERENCE/DOCKET NUMBER:  46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  617-523-3400
; TELEFAX:  617-523-6440
; TELEX:  <Unknown>
; INFORMATION FOR SEQ ID NO:  4:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4

Query Match      82.8%; Score 48; DB 9; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
Db      26 GYSFTDYNVY 35

RESULT 6
US-09-772-120-8
; Sequence 8, Application US/09772120
; Patent No. US20010014328A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
;             Graziano, Robert
;             Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
;             Comprised of Anti-Fc
;             {SYMBOL 97 \f "Symbol"} Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772.120
; FILING DATE: 26-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,011
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-064CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-772-120-8

Query Match      82.8%; Score 48; DB 10; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
```

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Db      45 GYSFTDYIIF 54

RESULT 7
US-09-217-268B-28
; Sequence 28, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Ep
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Us
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Murine R3 antibody
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: Deduced amino acid sequence of VH of murine R3 antibody
US-09-217-268B-28

Query Match      81.0%; Score 47; DB 10; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.56;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
Db      26 GYTFTNYIY 35

RESULT 8
US-09-217-268B-36
; Sequence 36, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Ep
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Us
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of humanized VH of murine R3 antibody cont
US-09-217-268B-36

Query Match      81.0%; Score 47; DB 10; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.56;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
Db      26 GYTFTNYIY 35

RESULT 9
US-10-194-975-11
; Sequence 11, Application US/10194975
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Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-11

Query Match 75.9%; Score 44; DB 9; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
||:|||||:
Db 26 GYTFTDYMH 35

RESULT 10

US-10-032-482-5
Sequence 5, Application US/10032482
Publication No. US20020197270A1
GENERAL INFORMATION:
APPLICANT: Cohen, Irun
APPLICANT: ROTTER, Varda
APPLICANT: Wolkowicz, Roland
APPLICANT: RUIZ, Pedro
APPLICANT: EREZ-ALON, Neta
APPLICANT: HERKEL, Johannes
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
TITLE OF INVENTION: IMMUNITY
FILE REFERENCE: COHEN42
CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: IL 121041
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 111
TYPE: PRT
ORGANISM: Mus musculus
US-10-032-482-5

Query Match 72.4%; Score 42; DB 9; Length 111;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:|||||:
Db 23 GYTFTDYMH 31

RESULT 11

US-09-929-665-20
Sequence 20, Application US/09929665
Publication No. US20030003101A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024

CURRENT APPLICATION NUMBER: US/09/929,665
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/357,704
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 125
TYPE: PRT
ORGANISM: Mus sp.
US-09-929-665-20

Query Match 72.4%; Score 42; DB 9; Length 125;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:|||||:
Db 26 GYTFTDYMH 34

RESULT 12

US-09-929-546-20
Sequence 20, Application US/09929546
Publication No. US20030031673A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
CURRENT APPLICATION NUMBER: US/09/929,546
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/357,708
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 125
TYPE: PRT
ORGANISM: Mus sp.
US-09-929-546-20

Query Match 72.4%; Score 42; DB 9; Length 125;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:|||||:
Db 26 GYTFTDYMH 34

RESULT 13

US-08-779-457-48
Sequence 48, Application US/08779457
Publication No. US20020193571A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

```
;
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-779-457-48

Query Match 72.4%; Score 42; DB 1; Length 249;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
||:|:| |:|
Db 26 GYTFTGYMY 35

RESULT 14
US-09-840-459-41
; Sequence 41, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-41

Query Match 70.7%; Score 41; DB 10; Length 98;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|:|:|:|:|
Db 26 GFTFSDYYMY 35

RESULT 15
US-09-144-886-63
; Sequence 63, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C25 region VH epitope 2
US-09-144-886-63
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Query Match 70.7%; Score 41; DB 9; Length 118;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|:|:|:|:|
Db 26 GFTFSDYYMY 35
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OM protein - protein search, using sw model

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Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

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Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

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Listing first 45 summaries

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3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	17	10	US-09-924-099-7
2	97	100.0	113	10	US-09-924-099-2
3	97	100.0	237	10	US-09-924-099-9
4	97	100.0	243	10	US-09-924-099-10
5	69	71.1	117	9	US-09-956-206A-76
6	69	71.1	117	9	US-09-956-206A-78
7	69	71.1	136	9	US-09-956-206A-47
8	69	71.1	136	9	US-09-956-206A-63
9	68	70.1	117	9	US-09-982-992A-6
10	66	68.0	117	9	US-09-726-258-48
11	66	68.0	117	9	US-09-726-258-49
12	66	68.0	125	9	US-09-929-665-20
13	66	68.0	125	9	US-09-929-546-20
14	66	68.0	135	9	US-09-726-258-37
15	66	68.0	253	9	US-09-726-258-44
16	66	68.0	253	9	US-09-726-258-52
17	66	68.0	253	9	US-09-726-258-55
18	66	68.0	256	9	US-09-726-258-70
19	66	68.0	298	9	US-09-726-258-60

20	66	68.0	452	9	US-09-726-258-71	Sequence 71, Appl
21	64	66.0	130	10	US-09-839-447A-3	Sequence 3, Appli
22	63	64.9	115	9	US-09-929-665-8	Sequence 8, Appli
23	63	64.9	115	9	US-09-929-546-8	Sequence 8, Appli
24	63	64.9	123	9	US-09-892-613C-18	Sequence 18, Appl
25	63	64.9	130	9	US-09-929-665-4	Sequence 4, Appli
26	63	64.9	130	9	US-09-929-546-4	Sequence 4, Appli
27	63	64.9	132	9	US-09-982-107-14	Sequence 14, Appl
28	63	64.9	140	9	US-09-905-928-6	Sequence 6, Appli
29	63	64.9	669	9	US-09-807-721-2	Sequence 2, Appli
30	61	62.9	152	10	US-09-881-823-20	Sequence 20, Appl
31	61	62.9	601	10	US-09-480-236-1	Sequence 1, Appli
32	60	61.9	98	9	US-10-194-975-6	Sequence 6, Appli
33	59	60.8	20	10	US-09-839-447A-32	Sequence 32, Appl
34	59	60.8	119	9	US-10-194-975-121	Sequence 121, App
35	59	60.8	672	9	US-09-900-766-1	Sequence 1, Appli
36	58	59.8	17	9	US-10-032-482-15	Sequence 15, Appl
37	58	59.8	17	10	US-09-861-294-15	Sequence 15, Appl
38	58	59.8	17	10	US-09-861-294-33	Sequence 33, Appl
39	58	59.8	17	10	US-09-910-059-31	Sequence 31, Appl
40	58	59.8	111	9	US-10-032-482-5	Sequence 5, Appli
41	58	59.8	117	9	US-10-194-975-118	Sequence 118, App
42	58	59.8	120	10	US-09-910-059-11	Sequence 11, Appl
43	58	59.8	120	10	US-09-910-059-55	Sequence 55, Appl
44	58	59.8	120	10	US-09-910-059-75	Sequence 75, Appl
45	58	59.8	120	10	US-09-910-059-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-924-099-7
; Sequence 7, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099,
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-7

Query Match 100.0%; Score 97; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
|||||
Db 1 DIDPYNGDTSYNQKFRD 17

RESULT 2
US-09-924-099-2
; Sequence 2, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori

```

; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-2

Query Match      100.0%; Score 97; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY * 1 DIDPYNGDTSYNQKFRD 17
      |||||
Db 50 DIDPYNGDTSYNQKFRD 66

RESULT 3
US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match      100.0%; Score 97; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
      |||||
Db 50 DIDPYNGDTSYNQKFRD 66

RESULT 4
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
```

```

; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match      100.0%; Score 97; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
      |||||
Db 50 DIDPYNGDTSYNQKFRD 66

RESULT 5
US-09-956-206A-76
; Sequence 76, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
;              CERIANI, ROBERTO L.
;              PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
;                   MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
;                   METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
```

; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-956-206A-76

Query Match 71.1%; Score 69; DB 9; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00054;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFRD 17
|:||||| | |||||:|
Db 51 INPYNGGTVYNQKFQD 66

RESULT 6
US-09-956-206A-78
; Sequence 78, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES

; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-956-206A-78
Query Match 71.1%; Score 69; DB 9; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00054;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFRD 17
|:||||| | |||||:|
Db 51 INPYNGGTVYNQKFQD 66

RESULT 7
US-09-956-206A-47
; Sequence 47, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES

; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-956-206A-47

Query Match 71.1%; Score 69; DB 9; Length 136;
Best Local Similarity 75.0%; Pred. No. 0.00063;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFRD 17
|:||||| | |||||:|

Db 70 INPYNGGTVYNQKFQD 85

RESULT 8

US-09-956-206A-63

; Sequence 63, Application US/09956206A

; Patent No. US20020164339A1

; GENERAL INFORMATION:

; APPLICANT: DO COUTO, FERNANDO J.R.

; CERIANI, ROBERTO L.

; PETERSON, JERRY A.

; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND

; METHODS OF HUMANIZING ANTIBODY PEPTIDES

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/956,206A

; FILING DATE: 19-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/525,539

; FILING DATE: 14-SEP-1995

; APPLICATION NUMBER: PCT/US95/11683

; FILING DATE: 14-SEP-1995

; APPLICATION NUMBER: 08/487,598

; FILING DATE: 7-JUNE-1995

; APPLICATION NUMBER: 08/307,868

; FILING DATE: 16-SEPT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: WITT, ERIC

; REGISTRATION NUMBER: 44,408

; REFERENCE/DOCKET NUMBER: 276332000101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 813-5600

; TELEFAX: (650) 494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 63:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 136 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 63:

US-09-956-206A-63

Query Match 71.1%; Score 69; DB 9; Length 136;

Best Local Similarity 75.0%; Pred. No. 0.00063;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFRD 17

I:|||||I|||||I

Db 70 INPYNGGTVYNQKFQD 85

RESULT 9

US-09-982-992A-6

; Sequence 6, Application US/09982992A

; Patent No. US20020164337A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M. et al.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE MAP PROTEIN AND METHOD OF USE IN TRB

; TITLE OF INVENTION: AND PREVENTING INFECTIONS

; FILE REFERENCE: P06922US02/BAS

; CURRENT APPLICATION NUMBER: US/09/982,992A

; CURRENT FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: 60/277,287

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/241,832

; PRIOR FILING DATE: 2000-10-20

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-982-992A-6

Query Match 70.1%; Score 68; DB 9; Length 117;

Best Local Similarity 68.8%; Pred. No. 0.00078;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFRD 17

|||||I|||||I

Db 51 IDPYDSETHYNQKFQD 66

RESULT 10

US-09-726-258-48

; Sequence 48, Application US/09726258

; Publication No. US20030021790A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc., Hsel, Vanessa

; APPLICANT: Koumenis, Iphigenia

; APPLICANT: Leong, Steven R.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Shahrokh, Zahra

; APPLICANT: Zapata, Gerardo A.

; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND

; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/726,258

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/234,182

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/094003

; FILING DATE: 24-JUL-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P1085R4-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-09-726-258-48

Query Match 68.0%; Score 66; DB 9; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.0016;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
||| ||:|:||||:
Db 51 IDPSNGETTYNQKFK 65

RESULT 11

US-09-726-258-49
; Sequence 49, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA: 09/234,182
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-726-258-49

Query Match 68.0%; Score 66; DB 9; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.0016;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
||| ||:|:||||:
Db 51 IDPSNGETTYNQKFK 65

RESULT 12

US-09-929-665-20
; Sequence 20, Application US/09929665

Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-20

Query Match 68.0%; Score 66; DB 9; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.0017;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
||:| || |||||:
Db 51 DINPGNGGTSYNQKFK 66

RESULT 13

US-09-929-546-20
; Sequence 20, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-20

Query Match 68.0%; Score 66; DB 9; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.0017;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
||:| || |||||:
Db 51 DINPGNGGTSYNQKFK 66

RESULT 14

US-09-726-258-37
; Sequence 37, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa


```
;
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-726-258-37

Query Match 68.0%; Score 66; DB 9; Length 135;
Best Local Similarity 73.3%; Pred. No. 0.0019;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 51 IDPSNGETTYNQKFK 65

RESULT 15
US-09-726-258-44
; Sequence 44, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
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; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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US-09-726-258-44

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Best Local Similarity 73.3%; Pred. No. 0.0036;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 74 IDPSNGETTYNQKFK 88

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 3.24138 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published_Applications-AA:*
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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	4	10	US-09-924-099-8 Sequence 8, Appli
2	21	100.0	7	9	US-09-968-561A-99 Sequence 99, Appl
3	21	100.0	7	10	US-09-192-854-61 Sequence 61, Appl
4	21	100.0	21	9	US-09-974-879-281 Sequence 281, App
5	21	100.0	24	9	US-10-164-359-11 Sequence 11, Appl
6	21	100.0	39	10	US-09-864-761-34201 Sequence 34201, A
7	21	100.0	45	10	US-09-864-761-44502 Sequence 44502, A
8	21	100.0	51	10	US-09-864-761-34507 Sequence 34507, A
9	21	100.0	53	10	US-09-764-877-1721 Sequence 1721, Ap
10	21	100.0	54	10	US-09-864-761-42767 Sequence 42767, A
11	21	100.0	57	10	US-09-764-877-1214 Sequence 1214, Ap
12	21	100.0	59	10	US-09-864-761-46881 Sequence 46881, A
13	21	100.0	65	10	US-09-867-550-1842 Sequence 1842, Ap
14	21	100.0	80	10	US-09-862-179A-26 Sequence 26, Appl
15	21	100.0	84	10	US-09-864-761-47725 Sequence 47725, A
16	21	100.0	87	10	US-09-764-860-427 Sequence 427, App
17	21	100.0	89	9	US-10-078-770-104 Sequence 104, App
18	21	100.0	89	9	US-10-078-770-112 Sequence 112, App
19	21	100.0	89	10	US-09-764-853-466 Sequence 466, App

20	21	100.0	100	9	US-09-974-879-279	Sequence 279, App
21	21	100.0	101	10	US-09-864-761-37100	Sequence 37100, A
22	21	100.0	106	10	US-09-925-297-790	Sequence 790, App
23	21	100.0	107	10	US-09-734-017A-36	Sequence 36, Appl
24	21	100.0	110	9	US-09-969-763-10	Sequence 10, Appl
25	21	100.0	113	10	US-09-924-099-2	Sequence 2, Appli
26	21	100.0	116	10	US-09-867-550-146	Sequence 146, App
27	21	100.0	117	9	US-09-906-209-6	Sequence 6, Appli
28	21	100.0	121	10	US-09-864-761-46883	Sequence 46883, A
29	21	100.0	125	10	US-09-764-898-245	Sequence 245, App
30	21	100.0	127	10	US-09-815-242-10432	Sequence 10432, A
31	21	100.0	128	10	US-09-764-870-277	Sequence 277, App
32	21	100.0	139	10	US-09-864-761-40558	Sequence 40558, A
33	21	100.0	143	9	US-09-925-299-1142	Sequence 1142, Ap
34	21	100.0	143	10	US-09-925-299-1142	Sequence 1142, Ap
35	21	100.0	148	10	US-09-908-711-91	Sequence 91, Appl
36	21	100.0	154	10	US-09-925-301-851	Sequence 851, App
37	21	100.0	156	10	US-09-870-756-6	Sequence 6, Appli
38	21	100.0	156	10	US-09-874-585B-6	Sequence 6, Appli
39	21	100.0	159	10	US-09-925-297-727	Sequence 727, App
40	21	100.0	167	9	US-09-738-626-4384	Sequence 4384, Ap
41	21	100.0	170	9	US-09-975-719-158	Sequence 158, App
42	21	100.0	176	12	US-10-062-254-230	Sequence 230, App
43	21	100.0	179	10	US-09-970-711-44	Sequence 44, Appl
44	21	100.0	180	10	US-09-864-761-37144	Sequence 37144, A
45	21	100.0	186	10	US-09-925-301-1414	Sequence 1414, Ap

ALIGNMENTS

RESULT 1
US-09-924-099-8
; Sequence 8, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR-FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-8

Query Match 100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
| | | |
Db 1 GLRF 4

RESULT 2
US-09-968-561A-99
; Sequence 99, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory

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; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-99

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GLRF 5

RESULT 3
US-09-192-854-61
; Sequence 61, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-61

Query Match          100.0%; Score 21; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
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Db 2 GLRF 5

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US-09-974-879-281
; Sequence 281, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13

; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
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; PRIOR APPLICATION NUMBER: US 09/511,939
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; ORGANISM: Homo sapiens
US-09-968-561A-99

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GLRF 5

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US-09-192-854-61
; Sequence 61, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-61

Query Match          100.0%; Score 21; DB 10; Length 7;
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Db 2 GLRF 5

RESULT 4
US-09-974-879-281
; Sequence 281, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
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; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
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; PRIOR APPLICATION NUMBER: US 60/064,900
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; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
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; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-281

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; GENERAL INFORMATION:
; APPLICANT: Chin, Khew-Voon
; TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement in Stress
; TITLE OF INVENTION: Stress
; FILE REFERENCE: 601-1-108US
; CURRENT APPLICATION NUMBER: US/10/164,359
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: PCT/US00/33438
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,418
; PRIOR FILING DATE: 1999-12-07
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Db 5 GLRF 8

RESULT 6
US-09-864-761-34201
; Sequence 34201, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
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; PRIOR APPLICATION NUMBER: US 09/608,408
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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.3e+02
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

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; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: P12114, EVALUE 6.20e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA336691.1, EVALUE 2.00e-16
US-09-864-761-34201

Query Match 100.0%; Score 21; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 25 GLRF 28

RESULT 7
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; Sequence 44502, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44502
; LENGTH: 45
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004108.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86
; OTHER INFORMATION: SWISSPROT HIT: Q09890, EVALUJE 4.80e+00
US-09-864-761-44502

Query Match 100.0%; Score 21; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 13 GLRF 16

RESULT 8

US-09-864-761-34507
; Sequence 34507, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34507
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006365.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
US-09-864-761-34507

Query Match 100.0%; Score 21; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 42 GLRF 45

RESULT 9

US-09-764-877-1721
; Sequence 1721, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1721
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (41)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1721

Query Match 100.0%; Score 21; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 35 GLRF 38

RESULT 10

US-09-864-761-42767
; Sequence 42767, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42767
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL035587.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3
; OTHER INFORMATION: SWISSPROT HIT: P17937, EVALUE 4.00e-04
; OTHER INFORMATION: EST_HUMAN HIT: BE409626.1, EVALUE 7.00e-25
US-09-864-761-42767

Query Match 100.0%; Score 21; DB 10; Length 54;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
Db 6 GLRF 9
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RESULT 11
US-09-764-877-1214
; Sequence 1214, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1214
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1214

Query Match 100.0%; Score 21; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
Db 32 GLRF 35
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RESULT 12
US-09-864-761-46881
; Sequence 46881, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46881
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000494.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EST_HUMAN HIT: AW270799.1, EVALUE 3.00e-04
; OTHER INFORMATION: SWISSPROT HIT: P12690, EVALUE 2.00e+00
US-09-864-761-46881

Query Match          100.0%; Score 21; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLRF 4
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Db      17 GLRF 20

RESULT 13
US-09-867-550-1842
; Sequence 1842, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1842
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1842

Query Match          100.0%; Score 21; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLRF 4
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Db      25 GLRF 28

RESULT 14
US-09-862-179A-26
; Sequence 26, Application US/09862179A
; Patent No. US20020147306A1
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; GENERAL INFORMATION:
; APPLICANT: Lin, Danny
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
; TITLE OF INVENTION: AND PDZ DOMAINS
; FILE REFERENCE: MTSI-P01-009
; CURRENT APPLICATION NUMBER: US/09/862,179A
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-179A-26

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLRF 4
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Db      39 GLRF 42

RESULT 15
US-09-864-761-47725
; Sequence 47725, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
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; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47725
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL033520.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EST_HUMAN HIT: BE897334.1, EVALUE 3.00e-10
US-09-864-761-47725

Query Match 100.0%; Score 21; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 16 GLRF 19

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OM protein - protein search, using sw model

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Title: US-09-924-099-6
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Sequence: 1 GYSFTDYFIY 10

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	58	100.0	237	21	AA44595
5	58	100.0	243	21	AA44596
6	53	91.4	242	23	ABP45974
7	53	91.4	242	23	ABP46088
8	50	86.2	120	22	AAB49746
9	50	86.2	253	23	ABP45515
10	49	84.5	112	23	AAE15811

11	49	84.5	114	23	AAG80197	Human gp96 Ab clon
12	48	82.8	117	19	AAW71288	Human anti-tissue
13	48	82.8	142	19	AAW48249	A77 anti-Fc alpha
14	48	82.8	142	22	AAE08555	Murine A77 anti-Fc
15	48	82.8	142	22	AAB74622	A77 anti-Fc-alpha-
16	48	82.8	353	20	AA406273	Anti Fc alpha rece
17	47	81.0	97	23	ABP01374	Human ORFX protein
18	47	81.0	122	22	AAG80211	Human autoantibody
19	47	81.0	123	17	AAR92992	Humanised antibody
20	47	81.0	123	17	AAR92990	Monoclonal antibody
21	47	81.0	249	23	ABP45719	Human BLYS binding
22	46	79.3	110	19	AAW39881	Heavy chain of the
23	46	79.3	116	19	AAW39889	Heavy chain of the
24	46	79.3	118	20	AA452755	Anti-tissue factor
25	46	79.3	118	20	AA452756	Anti-tissue factor
26	46	79.3	215	21	AAU78254	Mouse agglutinatio
27	46	79.3	245	23	ABP45889	Human BLYS binding
28	45	77.6	115	19	AAW39814	Variable domain of
29	45	77.6	116	17	AAW03742	Murine monoclonal
30	45	77.6	117	23	AAU99848	Mouse AC10 antibod
31	45	77.6	118	20	AA452760	Anti-tissue factor
32	45	77.6	118	20	AA430188	Amino acid sequenc
33	45	77.6	122	22	AAB62868	Anti-SAF-1 monoclo
34	45	77.6	137	19	AAW79226	Humanised LO-CD2a
35	45	77.6	137	19	AAW56350	Humanised LO-CD2a
36	45	77.6	137	20	AA430189	Amino acid sequenc
37	45	77.6	138	21	AA456873	MAB CT-M-01 heavy
38	45	77.6	139	14	AAAR33950	CTMO1 VH. Synthet
39	45	77.6	139	14	AAAR33953	gH1 variable domai
40	45	77.6	139	18	AAW29750	Anti-HMFG MAB CTMO
41	45	77.6	139	18	AAW29753	CDR-grafted human
42	45	77.6	139	21	AA456877	gH1 variable domai
43	45	77.6	251	23	ABP45325	Human BLYS binding
44	45	77.6	252	23	ABP45943	Human BLYS binding
45	45	77.6	255	23	ABP45396	Human BLYS binding

ALIGNMENTS

RESULT 1

AA44592

ID AA44592 standard; Protein; 10 AA.

XX AA44592;

XX 04-APR-2000 (first entry)

DT Mouse anti-IL-18 antibody VH complementarity-determining region-1.

DE Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;

XX complementarity-determining region; CDR; hybridoma #125-2H; mouse;

KW monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;

KW immunosuppressive; leucocytopenic; antialgic; antipyretic;

KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;

KW inflammatory disorder; immunoreaction.

XX Mus musculus.

XX EP974600-A2.

XX 26-JAN-2000.

XX 24-JUN-1999; 99EP-0304977.

XX 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.

PR 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PA Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49539.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 7; Page 18; 36pp; English.
XX
CC The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-Interleukin-18 antibody heavy chain variable region
CC (VH) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2HmAb, which is capable of neutralising biological activities of
CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
CC leukocytopenetic, antialgic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db |||||
1 GYSFTDYFIY 10

RESULT 2
AAAY44588
ID AAY44588 standard; Protein; 113 AA.
XX
AC AAY44588;
XX
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse anti-IL-18 antibody heavy chain variable region.
XX
KW Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;
KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
KW antiinflammatory; immunosuppressive; leukocytopenetic; antialgic;
KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
KW immunopathy; inflammatory disorder; immunoreaction.
XX
OS Mus musculus.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
XX WPI; 2000-118341/11.
DR N-PSDB; AAZ49535.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 5; Page 17-18; 36pp; English.
XX
CC The present protein sequence is the mouse anti-Interleukin-18 antibody

CC heavy chain variable region (VH) encoded by cDNA derived from hybridoma
CC #125-2H. The nucleotide sequence is used in the production of recombinant
CC monoclonal antibody #125-2HmAb, which is capable of neutralising
CC biological activities of interleukin-18. The antibody has antialgic,
CC antiinflammatory, immunosuppressive, leukocytopenetic, antipyretic,
CC antiallergic and hepatotropic activity and can be used for prevention and
CC treatment of autoimmune diseases, immunopathies and inflammatory
CC disorders caused by excessive immunoreaction.
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 58; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db |||||
26 GYSFTDYFIY 35

RESULT 3
AAAY44600
ID AAY44600 standard; Protein; 137 AA.
XX
AC AAY44600;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse heavy chain variable region encoded by PCR B product.
XX
KW Mouse heavy chain variable region; VH; variable region heavy chain;
KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
KW hematopoietic; leukocytopenetic; antialgic; antipyretic.
XX
OS Mus musculus.
OS Synthetic.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49549.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Disclosure; Page 29-30; 32pp; English.
XX
CC The present sequence is the mouse heavy chain variable region. This was
CC encoded by a recombinant DNA is derived from PCR B which amplifies
CC antibody heavy chain variable region (VH). The transformant produced
CC using the VH gene was used transform competent E. coli cells. The peptide
CC produced by transformants neutralises interleukin-18. This is useful for
CC treating and preventing immunopathies, inflammatory disorders and
CC autoimmune diseases which are caused by excessive immunoreaction. The
CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
CC hematopoietic, leukocytopenetic, antialgic, antipyretic and hepatic
CC -function improving activities.
XX
SQ Sequence 137 AA;

Query Match 100.0%; Score 58; DB 21; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
| | | | | | | | | |
Db 45 GYSFTDYFIY 54

RESULT 4
AAY44595
ID AAY44595 standard; Protein; 237 AA.
XX
AC AAY44595;
XX
DT 04-APR-2000 (first entry)
XX
DE EscFv#125-2H recombinant protein.
XX
KW EscFv#125-2H recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49542.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 8; Page 19-20; 32pp; English.
XX
CC The present sequence is EscFv#125-2H protein encoded by recombinant cDNA
CC pEscFv#125-2H for neutralising interleukin-18. The protein is produced
CC from hybridoma #125-2H by transforming pEscFv#125-2H in competent
CC E. coli cells. This is useful for treating and preventing immunopathies,
CC inflammatory disorders and autoimmune diseases which are caused by
CC excessive immunoreaction. The protein has anti-allergic,
CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,
CC antialgic, antipyretic and hepatic-function improving activities.
XX
SQ Sequence 237 AA;

Query Match 100.0%; Score 58; DB 21; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
| | | | | | | | | |
Db 26 GYSFTDYFIY 35

RESULT 5
AAY44596
ID AAY44596 standard; Protein; 243 AA.
XX
AC AAY44596;
XX
DT 04-APR-2000 (first entry)
XX
DE EscFv#125-2H.HT recombinant protein.
XX
KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49543.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 8; Page 20-21; 32pp; English.
XX
CC The present sequence is EscFv#125-2H.HT protein encoded by
CC recombinant cDNA pEscFv#125-2H.HT for neutralising interleukin-18. The
CC protein is produced from hybridoma #125-2H by transforming
CC pEscFv#125-2H.HT in competent E. coli cells. There are six histidine
CC residues positioned after the light chain variable region. This protein
CC is useful for treating and preventing immunopathies, inflammatory
CC disorders and autoimmune diseases which are caused by excessive
CC immunoreaction. The protein has anti-allergic, anti-inflammatory,
CC immunosuppressive, hematopoietic, leukocytopoietic, antialgic,
CC antipyretic and hepatic-function improving activities.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 58; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 GYSFTDYFIY 35

RESULT 6
ABP45974
ID ABP45974 standard; Protein; 242 AA.
XX
AC ABP45974;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1985.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
XX
PS Claim 1; Page 2769-2770; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 242 AA;

Query Match 91.4%; Score 53; DB 23; Length 242;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|||||||

Db 26 GYSFTDYFIH 35

RESULT 7
ABP46088
ID ABP46088 standard; Protein; 242 AA.
XX
AC ABP46088;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 2099.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
XX
PS Claim 1; Page 2901-2902; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 242 AA;

Query Match 91.4%; Score 53; DB 23; Length 242;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
|||||||

RESULT 8
AAB49746
ID AAB49746 standard; protein; 120 AA.
XX
AC AAB49746;
XX
DT 17-APR-2001 (first entry)
XX
DE Anti-PF4/heparin complex antibody heavy chain amino acid sequence.
XX
KW Antibody; platelet factor 4; heparin; PF4/heparin complex; mouse; HIT;
heparin induced thrombocytopaenia; heparin induced thrombosis; HITT.
XX
OS Mus musculus.
XX
PN WO200104159-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US19000.
XX
PR 13-JUL-1999; 99US-0143536.
XX
PA (SCTE-) SCI & TECHNOLOGY CORP @UNM.
XX
PI Arepally G, Kisiel W, Kamei K, Kamei S;
XX
DR WPI; 2001-138321/14.
DR N-PSDB; AAF29245.
XX
PT Composition for the diagnosis and treatment of heparin induced
PT thrombocytopenia/thrombosis, comprises an antibody that preferentially
PT binds with a Platelet Factor 4/heparin complex -
XX
PS Claim 5; Fig 7A; 80pp; English.
XX
CC This invention relates to a composition comprising a monoclonal antibody
CC which binds specifically with a Platelet Factor 4 (PF4)/heparin complex.
CC The antibody preferentially binds to the complex relative to the binding
CC of the antibody with either of the components alone. Methods are included
CC for the production of the antibody and its use in the diagnosis of
CC various diseases. The composition can be used for diagnosing heparin
CC induced thrombocytopaenia/thrombosis, HIT/HITT. The composition can also
CC be used for assessing the level of a polyclonal antibody that binds
CC specifically within a bodily fluid or tissue sample. The present sequence
CC represents the amino acid sequence of the heavy chain of the
CC anti-PF4/heparin complex antibody of the invention.
XX
SQ Sequence 120 AA;
Query Match 86.2%; Score 50; DB 22; Length 120;
Best Local Similarity 80.0%; Pred. NO. 0.33;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTDYFIY 10
Db 26 GYTFTNYFIY 35
RESULT 9
ABP45515
ID ABP45515 standard; Protein; 253 AA.
XX
AC ABP45515;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLYS binding scFv SEQ ID 1526.
XX
KW BLYS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
PT
XX Claim 1; Page 2224-2225; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
CC and so may be used to detect and quantitate the presence of BLYS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLYS. They may also be
CC administered to treat diseases associated with aberrant BLYS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 253 AA;
Query Match 86.2%; Score 50; DB 23; Length 253;
Best Local Similarity 80.0%; Pred. NO. 0.72;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTDYFIY 10
Db 26 GYSFTDYIYH 35
RESULT 10
AAE15811
ID AAE15811 standard; Protein; 112 AA.
XX
AC AAE15811;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human mAb 12B1 heavy chain variable region (VH).
XX
KW Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;
KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;
KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;

KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;
KW immunoglobulin; complementarity determining region; CDR; protozoacide;
KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;
KW fungicide; neuroprotective; heavy chain variable region; VH; mAb;
KW monoclonal antibody.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 31..35

FT /label= CDR

FT /note= "Complementarity determining region"

FT Region 50..66

FT /label= CDR

FT /note= "Complementarity determining region"

FT Region 99..102

FT /label= CDR

FT /note= "Complementarity determining region"

XX WO200190193-A1.

PN 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US16864.

XX 24-MAY-2000; 2000US-0577930.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Abrahamson JA, Kikly KK;

XX WPI; 2002-083094/11.

DR N-PSDB; AAD25486.

XX Novel monoclonal antibody that binds to human sialoadhesin factor-3 for
PT treating or preventing cancer, inflammation, autoimmunity, allergy,
PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections
PT .

XX Claim 20; Fig 1; 69pp; English.

XX The invention relates to monoclonal antibodies that bind to human
CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or
CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central
CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple
CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections
CC and for modulating an immune response in a mammal, where the immune
CC response is downregulated or enhanced. SAF-3 antibody is useful as
CC diagnostic and therapeutic reagents, to subcharacterise cell populations
CC during haematopoietic development, to treat anaemia, as a diagnostic
CC marker to distinguish between different forms of cancer, to purge bone
CC marrow ex vivo of cancer cells expressing SAF-3, as a tool to aid in the
CC ex vivo expansion (proliferation and/or differentiation) of
CC haematopoietic progenitor cells expressing SAF-3, as a stimulus in vivo
CC for stem cell mobilisation into the periphery and as an vivo
CC chemoprotective agent. Protein comprising immunoglobulin complementarity
CC determining region (CDR) of SAF-3 antibody and its nucleic acid is
CC useful to configure screening methods for detecting the effect of added
CC compounds on the production of mRNA and polypeptide in cells.
CC The present sequence is human monoclonal antibody (mAb) 12B1 heavy
CC chain variable region (VH) which binds to SAF-3.

XX SQ Sequence 112 AA;

Query Match 84.5%; Score 49; DB 23; Length 112;

Best Local Similarity 90.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10

|||||

Db 26 GYSFTDYNII 35

RESULT 11

AAG80197

ID AAG80197 standard; peptide; 114 AA.

XX AC AAG80197;

XX XX

DT 22-JAN-2002 (first entry)

XX XX

DE Human gp96 Ab clone G12D variable heavy chain framework region F1-FR4.

XX XX

KW Antibody; heavy chain; variable region; human; gp96; cytostatic;

KW framework region; antibacterial; virucide; fungicide; FR1; FR4;

KW protozoacide; tumour; autologous immunization; anti-idiotypic.

XX OS Homo sapiens.

XX PN DE10019967-A1.

XX PD 25-OCT-2001.

XX PF 20-APR-2000; 2000DE-1019967.

XX PR 20-APR-2000; 2000DE-1019967.

XX PA (FENN-) FENNING BIOMED GMBH.

XX PI Terness P, Kleist C, Opelz G, Welschof M, Arnold-Schild D;

PI Schild H, Rammensee H;

XX WPI; 2002-018649/03.

XX New recombinant antibody specific for native gp96, useful for isolating
PT gp96 as complex with endogenous peptides, used for autologous
PT immunotherapy of e.g. tumor
PT Claim 4; Page 15-16; 28pp; German.
XX This invention describes a novel recombinant antibody (Ab) that binds
CC native gp96. The product of the invention has cytostatic, antibacterial,
CC virucide, fungicide and protozoacide activity. Complexes of gp96 with the
CC peptides of the invention induce a immune response (cytotoxic T cells)
CC specific for the associated peptides. Ab are used for purification or
CC labeling of gp96, including intact complexes (C) with peptides (I), from
CC small amounts of tumour or infected cells. (C) are useful: (i) in human
CC or veterinary medicine for autologous immunization, for treating tumours
CC and infections (by viruses, bacteria, mycoplasma, fungi and parasites
CC (protozoa)); and (ii) for raising anti-idiotypic antibodies. Ab make
CC possible isolation of very pure gp96 in native form, even from small
CC tumour samples, in a one-step chromatographic process that does not
CC require concanavalin A (as used in known processes and which may
CC contaminate the final product by bleeding from the column). This sequence
CC represents the variable heavy chain framework region FR1-FR4 fragment
CC of the antibody raised against human gp96 described in the method of the
CC invention.

XX SQ Sequence 114 AA;

Query Match 84.5%; Score 49; DB 23; Length 114;

Best Local Similarity 70.0%; Pred. No. 0.46;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10

|||||

Db 26 GYFTDYMY 35

RESULT 12

AAW71288

ID AAW71288 standard; Protein; 117 AA.

XX AC AAW71288;

XX XX

DT 10-DEC-1998 (first entry)
XX
DE Human anti-tissue factor heavy chain variable region.
XX
KW Human; anti-tissue factor light chain variable region; H36.D2.B7;
KW anti-tissue factor heavy chain variable region; inhibition; antibody;
KW blood coagulation; thrombosis; restenosis; thromboembolic condition;
KW cardiovascular; infection; neoplastic disease; clot; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9840408-A1.
XX
PD 17-SEP-1998.
XX
PF 10-MAR-1998; 98WO-US04644.
XX
PR 10-MAR-1997; 97US-0814806.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Jiao J, Luepschen L, Nieves EL, Wong HC;
XX
DR WPI; 1998-520804/44.
DR N-PSDB; AAV54962.
XX
PT New antibody to human tissue factor - used for, e.g. treating
PT thrombosis or restenosis or thromboembolic conditions associated
PT with cardiovascular, infectious or neoplastic disease
XX
PS Claim 12; Fig 1B; 53pp; English.
XX
CC The present sequence represents the human anti-tissue factor heavy chain
CC variable region from an antibody that binds native human tissue factor
CC (TF) and does not bind non-native TF. The antibody capable of
CC specifically binding native TF may be used for inhibiting blood
CC coagulation and also for reducing TF levels in a mammal. The antibodies
CC can be used, e.g. to treat thromboses, particularly to prevent or
CC inhibit restenosis, or other thromboses following an invasive medical
CC procedure such as arterial or cardiac surgery (e.g. angioplasty,
CC endarterectomy, deployment of a stent, use of catheter, graft
CC implantation or use of an arteriovenous shunt). The antibodies can also
CC be used as a carrier for drugs, particularly pharmaceuticals targeted
CC for interaction with a blood clot such as streptokinase, tissue
CC plasminogen activator (t-PA) or urokinase, or a cytotoxic agent by
CC conjugating a suitable toxin to the antibody. Further the antibodies
CC can be used for treating a thromboembolic condition associated with
CC cardiovascular disease, an infectious disease, a neoplastic disease or
CC as a thrombolytic agent. The antibodies can also be used for detection
CC and diagnosis.
XX
SQ Sequence 117 AA;

Query Match 82.8%; Score 48; DB 19; Length 117;
Best Local Similarity 80.0%; Pred. NO. 0.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db ||||| : I
26 GYSFTDYNVY 35

RESULT 13
AAW48249
ID AAW48249 standard; Protein; 142 AA.
XX
AC AAW48249;
XX
DT 22-JUN-1998 (first entry)
XX
DE A77 anti-Fc alpha R antibody heavy chain variable VH region.
XX
KW A77 anti-Fc alpha R antibody; Fc-alpha receptor; antigen; cancer;

KW cytotoxic; white blood cell; infection.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9802463-A1.
XX
PD 22-JAN-1998.
XX
PF 10-JUL-1997; 97WO-US12013.
XX
PR 11-JUL-1996; 96US-0678194.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Keler T;
XX
DR WPI; 1998-110533/10.
DR N-PSDB; AAV20602.
XX
PT Multispecific binding molecules reactive with Fc-alpha receptor and
PT antigen - for treatment and prevention of cancer and infections by
PT activating cytotoxic potential of Fc-alpha on white blood cells
XX
PS Claim 18; Page 61-62; 106pp; English.
XX
CC The present sequence represents A77 anti-Fc alpha R antibody heavy chain
CC variable VH region, which is used to produce the humanised determinant
CC in a bi-specific binding molecule of the present invention. The present
CC invention describes a bi- or multi-specific binding molecule (I)
CC comprising a first binding determinant (BD1) which binds a Fc alpha
CC receptor and a second BD (BD2) that binds to at least one antigen (Ag).
CC (I) are used: (i) to eliminate/reduce unwanted cells in a subject (human
CC or animal); (ii) to vaccinate against pathogens (specifically Candida
CC but many others disclosed including hepatitis and human immune
CC deficiency viruses); (iii) to arm effector cells against pathogens or
CC cancer cells. Ag may also be an allergen. (I) exploits the cytotoxic
CC (cytolytic and phagocytic) potential of Fc alpha on white blood cells,
CC improving their on cancer/infected cells. When used in vaccines, (I) may
CC reduce the amount of antigen needed, and may be effective in patients
CC who do not respond well to antigen.
XX
SQ Sequence 142 AA;

Query Match 82.8%; Score 48; DB 19; Length 142;
Best Local Similarity 80.0%; Pred. NO. 0.86;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db ||||| : I
45 GYSFTDYIIF 54

RESULT 14
AAE08555
ID AAE08555 standard; Protein; 142 AA.
XX
AC AAE08555;
XX
DT 15-NOV-2001 (first entry)
XX
DE Murine A77 anti-Fc alpha R antibody heavy chain variable region.
XX
KW Murine; multispecific binding molecule; Fc alpha receptor; antibody A77;
KW cytolysis; phagocytosis; white blood cell; therapy; cancer; testicular;
KW breast; ovarian; prostate; lung; brain; colon; lymphatic system; vaccine;
KW human immunodeficiency virus; pathogenic infection; Toxoplasma gondii;
KW Candida albicans; Staphylococcus aureus; Staphylococcus haemolyticus;
KW Mycobacterium tuberculosis; immune response; chronic infection; anti-HIV;
KW hepatitis; autoimmune disease; acquired immunodeficiency syndrome; AIDS;
KW heavy chain variable region; VH; cytostatic; fungicide; virucide;
KW bactericide; protozoacide; hepatotropic; anti-inflammatory;
KW immunostimulant.

XX Mus sp.
OS US2001014328-A1.
XX 16-AUG-2001.
XX 26-JAN-2001; 2001US-0772120.
XX 10-JUL-1997; 97US-0890011.
PR 11-JUL-1996; 96US-0678194.
XX (MEDE-) MEDERAX INC.
XX Deo YM, Graziano R, Keler T;
PI WPI; 2001-529092/58.
XX N-PSDB; AAD15263.
DR
XX New multispecific binding molecule, useful for treating cancer and
PT infections caused by bacteria, virus, fungi or protozoa, comprises
PT binding determinant for Fc alpha receptor and binding determinant for
PT target antigen -
XX
XX Claim 18; Fig 28; 54pp; English.
XX
XX The present invention relates to multispecific binding molecules,
CC comprising a first binding determinant which binds an Fcalpha receptor,
CC or a functional fragment of antibody A77 and a second binding
CC determinant which binds one or more target antigens on a cancer cell or
CC on a pathogen (infected cell). The specific and multispecific molecules
CC can be used as therapeutic agents to harness the cytotoxicity and
CC phagocytosis capabilities of white blood cells, enhancing the attack of
CC these cells against cancer cells, cells of infectious microorganisms and
CC cells infected with pathogens. The multispecific binding molecules may
CC also be used to treat variety of diseases such as cancer (e.g. breast,
CC ovarian, testicular, prostate, lung, brain, colon or lymphatic system),
CC pathogenic infections such as viral (human immunodeficiency virus),
CC protozoan (e.g. Toxoplasma gondii), fungal (e.g. Candida albicans) and
CC bacterial (e.g. Staphylococcus aureus, S. haemolyticus and
CC Mycobacterium tuberculosis) and autoimmune diseases. These may also be
CC used as vaccine against diseases and cancer antigen or cancer found on
CC a pathogen or a cell infected by a pathogen. The methods can be used to
CC enhance or reinforce the immune response to an antigen, for the
CC treatment of acute and chronic infections, such as hepatitis and
CC acquired immunodeficiency syndrome (AIDS). The present sequence is
CC murine heavy chain variable (VH) region of A77 anti-FcalphaR antibody.
XX
SQ Sequence 142 AA;
Query Match 82.8%; Score 48; DB 22; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYSFTDYFIY 10
Db 45 GYSFTDYIIF 54
RESULT 15
AAB74622
ID AAB74622 standard; Protein; 142 AA.
XX
AC AAB74622;
XX
DT 22-MAY-2001 (first entry)
XX
DE A77 anti-Fc-alpha-R antibody VH region protein SEQ ID NO:8.
XX
KW Murine; human; immunoglobulin G1; IgG1; A77. anti-Fc-alpha-R antibody;
KW cytotostatic; antibacterial; antifungal; antiviral; antiparasitic;
KW cancer; pathogen; infection; vaccine.
XX

OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN US6193966-B1.
XX 27-FEB-2001.
XX
PD
XX 10-JUL-1997; 97US-0890011.
PF
XX 11-JUL-1996; 96US-0678194.
PR
XX (MEDE-) MEDERAX INC.
PA
XX Deo YM, Graziano R, Keler T;
PI WPI; 2001-243397/25.
XX N-PSDB; AAF74892.
DR
XX Selectively eliminating cancer cell in vivo by administering bispecific
PT protein comprising binding determinants that bind Fcalpha receptor
PT without being blocked by IgA and target antigen, respectively on the
PT cell -
XX
XX Claim 16; Column 47-50; 55pp; English.
PS
XX The present invention describes a method for selectively eliminating a
CC cell in a subject involving administering a bispecific protein or peptide
CC (I) comprising first and second binding determinants (BD1, BD2) which
CC bind to the Fc-alpha receptor (FCR) without being blocked by
CC immunoglobulin A (IgA), and target antigen (Ag) on the cell,
CC respectively. (I) has cytostatic, antibacterial, antifungal, antiviral
CC and antiparasitic activities, and can be used for the selective
CC elimination of cancer cells and pathogen infected cells, and in vaccine
CC production. The method selectively eliminates a cell, a cancer cell from
CC cancers of breast, ovary, testis, lung, colon, rectum, pancreas, liver,
CC central nervous system, head and neck, kidney, bone, blood or lymphatic
CC system by administering (I) which comprises BD1 that binds to FCR, and
CC BD2 that binds to a target antigen, a cancer cell antigen such as a
CC member of the human epidermal growth factor (EGF)-like receptor family,
CC preferably an EGF receptor. Alternately, BD2 binds to the cancer cell
CC antigen such as HER-2/neu or HER-3, HER-4, a heterodimeric receptor
CC comprised of at least one HER subunit, or a cancer cell antigen such as
CC carcinoembryonic antigen, gastrin releasing peptide receptor antigen or
CC mucine tumour antigen TAG72. Optionally BD2 of (I) binds to a target
CC antigen, an antigen from a pathogen (bacteria, fungi (preferably
CC Candida sp., protozoa or virus) infected cell. (I) which comprises BD1
CC and an antigen, preferably from disease organisms, infected cells, from
CC gene products of disease organisms or from cancer cells is useful for
CC vaccination purposes against diseases and cancers. The present sequence
CC represents the A77 anti-Fc-alpha-R antibody VH region, which is given in
CC the exemplification of the present invention.
XX
SQ Sequence 142 AA;
Query Match 82.8%; Score 48; DB 22; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYSFTDYFIY 10
Db 45 GYSFTDYIIF 54
Search completed: March 10, 2003, 16:56:57
Job time : 29.2759 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 48.069 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	17	21 AAY44593	Mouse anti-IL-18 a
2	97	100.0	113	21 AAY44588	Mouse anti-IL-18 a
3	97	100.0	137	21 AAY44600	Mouse heavy chain
4	97	100.0	237	21 AAY44595	EscFv#125-2H recom
5	97	100.0	243	21 AAY44596	EscFv#125-2H.HT re
6	76	78.4	110	20 AAW84099	Vitronectin alpha-
7	76	78.4	117	20 AAW84093	Murine vitronectin
8	76	78.4	117	20 AAW84097	Humanised anti-alp
9	74	76.3	236	15 AAR45442	Sequence of the si
10	74	76.3	237	17 AAR94020	Anti-erbB2 scfv.

11	74	76.3	237	18 AAW15185	Single-chain anti-
12	74	76.3	237	21 AAY79059	Amino acid sequenc
13	71	73.2	17	23 AAE15814	Human mAb 12B1 VH
14	71	73.2	98	13 AAR27008	Hypercalcaemia age
15	71	73.2	108	16 AAR79243	Heavy chain variab
16	71	73.2	112	23 AAE15811	Human mAb 12B1 hea
17	71	73.2	116	13 AAR27010	Hypercalcaemia age
18	71	73.2	116	18 AAW22418	Reshaped human AUK
19	71	73.2	135	13 AAR29016	pUC-RVh-1220b. Sy
20	71	73.2	135	13 AAR29017	pUC-RVh-1220d. Sy
21	71	73.2	135	13 AAR28669	p12-h2. Synthetic
22	70	72.2	119	13 AAR25730	Humanised VH regio
23	70	72.2	119	22 AAB69679	Murine CMV5 antibo
24	70	72.2	119	22 AAB69680	Humanised CMV5 ant
25	70	72.2	119	22 AAB69692	Human Wol antibody
26	70	72.2	138	22 AAB69688	Murine CMV5 antibo
27	70	72.2	243	15 AAR60781	Fv(GP-4) immunosup
28	69	71.1	118	20 AAY52755	Anti-tissue factor
29	69	71.1	118	20 AAY52756	Anti-tissue factor
30	69	71.1	118	20 AAY52759	Anti-tissue factor
31	69	71.1	118	20 AAY52760	Anti-tissue factor
32	69	71.1	120	22 AAG78737	Phosphonate, ester
33	69	71.1	136	17 AAW06446	HuMc3 VH region BR
34	69	71.1	136	17 AAW06442	HuMc3 VH region.
35	68	70.1	17	22 AAB62862	Anti-SAF-1 antibod
36	68	70.1	17	23 AAU72832	Anti-NKG2D hybrido
37	68	70.1	117	23 AAU72830	Anti-NKG2D hybrido
38	68	70.1	120	22 AAB62860	Anti-SAF-1 monoclo
39	68	70.1	273	15 AAR52865	Anti-influenza N10
40	68	70.1	507	23 AAU72858	8G7c10x4-7 bispeci
41	67	69.1	115	19 AAW39812	Variable domain of
42	67	69.1	119	20 AAY21819	11E10 antibody hea
43	67	69.1	129	13 AAR25959	ICAM-1 inhibiting
44	67	69.1	139	14 AAR38259	Chimeric 128.1 VH,
45	67	69.1	153	12 AAR11597	Murine monoclonal

ALIGNMENTS

RESULT 1

AAV44593

ID AAY44593 standard; Protein; 17 AA.

XX AAY44593;

DT 04-APR-2000 (first entry)

XX Mouse anti-IL-18 antibody VH complementarity-determining region-2.

DE Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;

XX complementarity-determining region; CDR; hybridoma #125-2H; mouse;

KW monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;

KW immunosuppressive; leucocytopenietic; antialgic; antipyretic;

KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;

KW inflammatory disorder; immunoreaction.

XX Mus musculus.

XX EP974600-A2.

XX 26-JAN-2000.

XX 24-JUN-1999; 99EP-0304977.

XX 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.

PR 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49540.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
XX
PS Claim 7; Page 19; 36pp; English.
XX
CC The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-Interleukin-18 antibody heavy chain variable region
CC (VH) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2HmAb, which is capable of neutralising biological activities of
CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
CC leucocytopenetic, antialgic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 97; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
Db | | | | | | | | | | | | | | | | | | | |
1 DIDPYNGDTSYNQKFRD 17

RESULT 2
AAY44588
ID AAY44588 standard; Protein; 113 AA.
XX
AC AAY44588;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse anti-IL-18 antibody heavy chain variable region.
XX
KW Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;
KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
KW antiinflammatory; immunosuppressive; leucocytopenetic; antialgic;
KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
KW immunopathy; inflammatory disorder; immunoreaction.
XX
OS Mus musculus.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49535.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 5; Page 17-18; 36pp; English.
XX
CC The present protein sequence is the mouse anti-Interleukin-18 antibody

CC heavy chain variable region (VH) encoded by cDNA derived from hybridoma
CC #125-2H. The nucleotide sequence is used in the production of recombinant
CC monoclonal antibody #125-2HmAb, which is capable of neutralising
CC biological activities of interleukin-18. The antibody has antialgic,
CC antiinflammatory, immunosuppressive, leucocytopenetic, antipyretic,
CC antiallergic and hepatotropic activity and can be used for prevention and
CC treatment of autoimmune diseases, immunopathies and inflammatory
CC disorders caused by excessive immunoreaction.
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 97; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
Db | | | | | | | | | | | | | | | | | | | |
50 DIDPYNGDTSYNQKFRD 66

RESULT 3
AAY44600
ID AAY44600 standard; Protein; 137 AA.
XX
AC AAY44600;
XX
DT 04-APR-2000 (first entry)
XX
DE Mouse heavy chain variable region encoded by PCR B product.
XX
KW Mouse heavy chain variable region; VH; variable region heavy chain;
KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
KW hematopoietic; leucocytopenetic; antialgic; antipyretic.
XX
OS Mus musculus.
OS Synthetic.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49549.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Disclosure; Page 29-30; 32pp; English.
XX
CC The present sequence is the mouse heavy chain variable region. This was
CC encoded by a recombinant DNA is derived from PCR B which amplifies
CC antibody heavy chain variable region (VH). The transformant produced
CC using the VH gene was used transform competent E. coli cells. The peptide
CC produced by transformants neutralises interleukin-18. This is useful for
CC treating and preventing immunopathies, inflammatory disorders and
CC autoimmune diseases which are caused by excessive immunoreaction. The
CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
CC hematopoietic, leucocytopenetic, antialgic, antipyretic and hepatic
CC -function improving activities.
XX
SQ Sequence 137 AA;

Query Match 100.0%; Score 97; DB 21; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
|||||
Db 69 DIDPYNGDTSYNQKFRD 85

RESULT 4
AAY44595
ID AAY44595 standard; Protein; 237 AA.
XX
AC AAY44595;
XX

DT 04-APR-2000 (first entry)

XX EscFv#125-2H recombinant protein.

DE EscFv#125-2H recombinant protein; interleukin-18; mouse;
XX immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX Mus musculus.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"

XX EP974600-A2.

PN 26-JAN-2000.

XX 24-JUN-1999; 99EP-0304977.

PR 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.

PR 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

DR N-PSDB; AAZ49542.

XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX Claim 8; Page 19-20; 32pp; English.

PS The present sequence is EscFv#125-2H protein encoded by recombinant cDNA
CC pEscFv#125-2H for neutralising interleukin-18. The protein is produced
CC from hybridoma #125-2H by transforming pEscFv#125-2H in competent
CC E. coli cells. This is useful for treating and preventing immunopathies,
CC inflammatory disorders and autoimmune diseases which are caused by
CC excessive immunoreaction. The protein has anti-allergic,
CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,
CC antialgic, antipyretic and hepatic-function improving activities.

XX Sequence 237 AA;

Query Match 100.0%; Score 97; DB 21; Length 237;
Best Local Similarity 100.0%; Pred. No. 8.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
|||||
Db 50 DIDPYNGDTSYNQKFRD 66

RESULT 5
AAY44596
ID AAY44596 standard; Protein; 243 AA.
XX
AC AAY44596;
XX

DT 04-APR-2000 (first entry)

XX EscFv#125-2H.HT recombinant protein.

DE EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
XX immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX Mus musculus.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"

XX EP974600-A2.

PN 26-JAN-2000.

XX 24-JUN-1999; 99EP-0304977.

PR 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.

PR 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

DR N-PSDB; AAZ49543.

XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX Claim 8; Page 20-21; 32pp; English.

PS The present sequence is EscFv#125-2H.HT protein encoded by
CC recombinant cDNA pEscFv#125-2H.HT for neutralising interleukin-18. The
CC protein is produced from hybridoma #125-2H by transforming
CC pEscFv#125-2H.HT in competent E. coli cells. There are six histidine
CC residues positioned after the light chain variable region. This protein
CC is useful for treating and preventing immunopathies, inflammatory
CC disorders and autoimmune diseases which are caused by excessive
CC immunoreaction. The protein has anti-allergic, anti-inflammatory,
CC immunosuppressive, hematopoietic, leukocytopoietic, antialgic,
CC antipyretic and hepatic-function improving activities.

XX Sequence 243 AA; ✓

Query Match 100.0%; Score 97; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17


```

Db      50 DIDPYNGDTSYNQKFRD 66
|||||

```

RESULT 6
AAW84099
ID AAW84099 standard; Protein: 110 AA.

Humanised antibody; monoclonal antibody; MAb; antibody engineering;
mouse; human; vitronectin; alpha v beta-3; receptor; restenosis;
cancer; metastasis; rheumatoid arthritis; atherosclerosis;
angiogenesis; diabetic retinopathy; inflammation;
macular degeneration; osteoporosis; Paget's disease;
hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

New anti alpha_v beta_3 vitronectin receptor antibodies - used for immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or osteoporosis

PS Example 13; Page 63; 97pp; English.

This is the amino acid sequence of the region of the murine monoclonal antibody (MAb) D12 heavy chain variable region (VH) that is altered in humanised D12 VH (see also AAW84097). A synthetic gene (see AAV81901) encoding the protein was prepared from synthetic oligonucleotides and used to prepare an expression vector for humanised D12 VH. D12 is an anti-human alpha-v beta-3 vitronectin receptor MAb. Humanised D12 MAbs can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis and angiogenic associated diseases.

Sequence 110 AA; SQ

Query Match	78.4%;	Score 76;	DB 20;	Length 110;
Best Local Similarity	86.7%;	Pred. No. 9.5e-05;		
Matches . 13;	Conservative	1;	Mismatches 1;	Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFR 16
 |||||
 Db 49 IDPYNGDTSYNQKFK 63

RESULT 7
AAW84093
ID AAW84093 standard; Protein: 117 AA.

DT	15-MAR-1999	(first entry)
XX		
DE	Murine vitronectin alpha-v beta-3 receptor MAb VH region.	
XX		
KW	Humanised antibody; monoclonal antibody; MAb; antibody engineering;	
KW	mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;	
KW	cancer; metastasis; rheumatoid arthritis; atherosclerosis;	
KW	angiogenesis; diabetic retinopathy; inflammation;	
KW	macular degeneration; osteoporosis; Paget's disease;	
KW	hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.	
XX		
OS	Mus sp.	
XX		
Key	Location/Qualifiers	
FT	Region	31..35
FT		/label= CDR1
FT	Region	50..66
FT		/label= CDR2
FT	Region	99..106
FT		/label= CDR3
XX		
PN	WO9840488-A1.	
XX		
PD	17-SEP-1998.	
XX		
PF	12-MAR-1998;	98WO-US04987.
XX		
PR	12-MAR-1997;	97US-0039609.
XX		
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX		
PI	Johanson KO, Jonak ZL, Taylor AH;	
XX		
DR	WPI; 1999-034590/03.	
XX		
PT	New anti alpha_v beta_3 vitronectin receptor antibodies - used for	
PT	immunotherapeutic treatment of e.g. diabetic retinopathy,	
PT	inflammatory disorders, atherosclerosis, restenosis, cancers or	
PT	osteoporosis	
XX		
PS	Example 13; Page 56; 97pp; English.	

This is the amino acid sequence of the heavy chain variable region (VH) of the anti-human alpha-v beta-3 vitronectin receptor murine monoclonal antibody D12, as deduced from isolated cDNA (see AAV71797). D12 VH and VL (see AAW84094) show sequence similarity to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see AAW84096), respectively. Humanised VH (see AAW84097) and VL (see AAW84098) were constructed by combining the framework regions of the human v region consensus sequences with complementarity determining regions of D12 (keeping some preferred murine framework residues). The humanised antibodies are specifically reactive with the human alpha-v beta-3 protein receptor and capable of neutralising the receptor. They can be used for passive immunotherapy of a disorder mediated by the alpha-v beta-3 receptor, e.g. cardiovascular disorders or angiogenic-related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and restenosis, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy, osteolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex hormone deficiency. They can also be used for targeted drug therapy, and for detection and diagnosis.

Sequence	117 AA;
SQ	

Query Match	78.4%;	Score 76;	DB 20;	Length 117;
Best Local Similarity	86.7%;	Pred. No. 0.0001;		
Matches 13;	Conservative 1;	Mismatches 1;	Indels	

Qy 2 IDPYNGDTSYNQKFR 16
|||||||

Db 51 IDPYNGDTFYNQKFK 65

RESULT 8
AAW84097

ID AAW84097 standard; Protein; 117 AA.
XX
AC AAW84097;
XX

DT 15-MAR-1999 (first entry)
XX
DE Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VH.
XX

KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12HZHC-10.
XX

OS Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
FT Region 99..106
FT /label= CDR3
XX

PN WO9840488-A1.
XX

PD 17-SEP-1998.
XX

PF 12-MAR-1998; 98WO-US04987.
XX

PR 12-MAR-1997; 97US-0039609.
XX

PA (SMIK) SMITHKLINE BEECHAM CORP.
XX

PI Johanson KO, Jonak ZL, Taylor AH;
XX

DR WPI; 1999-034590/03.
DR N-PSDB; AAV71799.
XX

PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis
XX

PS Claim 1; Page 58; 97pp; English.
XX

CC This is the amino acid sequence of the heavy chain variable region
CC (VH) of humanised anti-alpha-v beta-3 vitronectin receptor
CC monoclonal antibody D12HZHC 1-0. It is based on the VH sequence
CC (see AAW84095) of human Kabat subgroup I VH, with complementarity
CC determining regions (CDRs) from the murine anti-human alpha-v
CC beta-3 vitronectin receptor monoclonal antibody D12 (see AAW84093).
CC 7 Murine framework residues (24, 48, 67, 68, 70, 72 and 74)
CC are retained. The humanised heavy chain can be expressed in host
CC cells using nucleic acid molecules (see AAV71799) of the invention.
CC Humanised D12 VL is also provided (see AAW84098)). The humanised
CC antibodies can be used for passive immunotherapy of disorders
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
CC angiogenic-related disorders, such as angiogenesis associated
CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
CC inflammatory disorders, macular degeneration, rheumatoid arthritis
CC and cancer, e.g. solid tumour metastasis, and diseases where bone
CC resorption is associated with pathology such as osteoporosis,
CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
CC osteolytic lesions produced by bone metastasis, bone loss due to

CC immobilisation or sex hormone deficiency. They can also be used for
CC targeted drug therapy, and for detection and diagnosis.
XX

SQ Sequence 117 AA;
Query Match 78.4%; Score 76; DB 20; Length 117;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:|||||:||||:
Db 51 IDPYNGDTFYNQKFK 65

RESULT 9
AAR45442
ID AAR45442 standard; Protein; 236 AA.
XX
AC AAR45442;
XX

DT 21-JUL-1994 (first entry)
XX

DE Sequence of the single chain anti-erbB2 antibody, Ab no.23.
XX

KW Single chain anti-erbB1 antibody; cancer therapy; prevention;
KW monoclonal antibody.
XX

OS Synthetic.
XX

PN WO9400136-A.
XX

PD 06-JAN-1994.
XX

PF 21-OCT-1992; 92WO-US08545.
XX

PR 30-JUN-1992; 92US-0906555.
XX

PA (MOLE-) MOLECULAR ONCOLOGY INC.
XX

PI Kasprzyk PG, King CR;
XX

DR WPI; 1994-025878/03.
DR N-PSDB; AAR455180.
XX

PT Treatment of malignancies over-expressing ERB-{2 - using at least
PT 2 monoclonal antibodies which recognise different epitopes on
PT gp185
XX

PS Example; Fig 7; 37pp; English.
XX

CC The source of human erbB-2 protein for the prodn. of antibodies no.
CC 23 and 21 (AAQ55180/R45442; AAQ55181/R45443) is a NIH/3T3 cell
CC engineered to express the human erbB-2 protein on its surface (N/
CC erbB-2). Abs no. 21 and 23 are directed against the extracellular
CC domain of gp185 erbB-2. Nude mice manipulated to produce rapidly
CC growing tumours were used in a trial of the efficacy of the Abs. In
CC animals given a combination of the 2 Abs, tumours completely
CC regressed after 11 days.
XX

SQ Sequence 236 AA;
Query Match 76.3%; Score 74; DB 15; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.00047;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:|||||:||||:
Db 170 INPYNGDTNYNQKFK 184

RESULT 10
AAR94020
ID AAR94020 standard; Protein; 237 AA.

```
XX AAR94020;
AC
XX
XX 21-MAY-1996 (first entry)
XX
XX Anti-erbB2 scFv.
DE
XX
XX Oncoprotein; erbB2; cell proliferation; tumour; cancer;
KW intracellular antibody homologue; single chain antibody; scFv;
KW gene therapy.
XX
XX Synthetic.
OS
XX WO9607321-A1.
PN
XX
XX 14-MAR-1996.
PD
XX
XX 23-AUG-1995; 95WO-US10740.
PF
XX
XX 06-JUN-1995; 95US-0468252.
PR
XX 06-SEP-1994; 94US-0301339.
PR
XX (UABR-) UAB RES FOUND.
PA
XX
XX Curiel DT, Deshane J;
PI
XX
XX WPI; 1996-171307/17.
DR
XX N-PSDB; AAT17728.
DR
XX
XX Inhibition of proliferation or survival of, esp. malignant erbB2,
PT cells - by introducing nucleic acid mol. encoding antibody homologue
PT which is expressed and binds, pref. erbB2, protein intracellularly
XX
XX Disclosure; Page 29-30; 48pp; English.
PS
XX
XX A nucleic acid comprises a first sequence encoding a signal peptide
CC (AAR94019) linked to a second sequence (AAT17728) encoding a single
CC chain Fv fragment (AAR94020) that binds a human erbB2 oncoprotein.
CC The anti-erbB2 scFv portion is obtained by PCR using e23scFv
CC plasmid as template. The signal peptide directs the scFv to the
CC endoplasmic reticulum. The nucleic acid is incorporated into a
CC plasmid or viral vector to facilitate expression of the scFv antibody
CC homologue within e.g. an epithelial carcinoma cell. Intracellular
CC expression of the homologue inhibits surface expression of erbB2 and
CC thereby inhibits cell proliferation and cell survival and decreases
CC tumorigenicity.
XX
XX Sequence 237 AA;
SQ
Query Match 76.3%; Score 74; DB 17; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFR 16
Db 171 INPYNGDTNYNQKFK 185
|:|||||:|||||:
RESULT 11
AAW15185
ID AAW15185 standard; Protein; 237 AA.
XX
XX AAW15185;
AC
XX
XX 05-JUN-1997 (first entry)
DT
XX Single-chain anti-erbB2 antibody e23(Fv).
DE
XX
XX Single chain antibody; variable region; light chain; heavy chain;
KW breast cancer; ovarian cancer; non-small cell lung carcinoma;
KW immunodiagnosis; treatment; cytotoxic agent; erbB-2.
XX
XX Mus musculus.
OS
```

```
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 108..121
FT /label= linker
FT
XX
XX US5587458-A.
PN
XX
XX 24-DEC-1996.
PD
XX
XX 07-OCT-1991; 91US-0772270.
PF
XX
XX 14-MAY-1993; 93US-0061092.
PR
XX 07-OCT-1991; 91US-0772270.
PR
XX 30-JUN-1992; 92US-0906555.
PR
XX
XX (ARON-) ARONEX PHARM INC.
PA
XX
XX Bird RE, Kasprzyk PG, King CR;
PI
XX WPI; 1997-064831/06.
PR
XX N-PSDB; AAT65006.
DR
XX
XX Single chain antibodies specific for erbB-2 protein, gp185 - with
PT labels or cytotoxin, useful for detection and treatment of tumour
PT cells expressing this protein
PT
XX
XX Claim 2; Columns 25-28; 28pp; English.
PS
XX
XX The present sequence represents a claimed single-chain antibody,
CC designated e23(Fv), which binds to erbB-2. Monoclonal antibody e23
CC was generated by immunising mice with N/erbB-2 cells overexpressing
CC the gp185 protein, removing spleen cells and producing hybridomas
CC by standard techniques. Messenger RNA coding for the anti-erbB-2
CC monoclonal antibody was isolated and converted to cDNA. Regions
CC coding for the heavy- and light- chain variable regions were then
CC amplified by PCR and joined via a sequence encoding a peptide
CC linker. The resulting single-chain antibody is useful for in vitro
CC diagnosis of tumour cells which overexpress the erbB-2 gp185
CC marker, e.g. breast, ovarian and non-small cell lung carcinomas,
CC and, when coupled to a cytotoxic agent, to treat such tumours.
XX
XX Sequence 237 AA;
SQ
Query Match 76.3%; Score 74; DB 18; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00048;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFR 16
Db 171 INPYNGDTNYNQKFK 185
|:|||||:|||||:
RESULT 12
AAW79059
ID AAW79059 standard; Protein; 237 AA.
XX
XX AAW79059;
AC
XX
XX 20-JUN-2000 (first entry)
DT
XX
XX Amino acid sequence of anti-erbB2 scFv.
DE
XX
XX Anti-erbB2 scFv; erbB2; proliferation; cell death; cancer;
KW epithelial carcinoma; breast; ovary; gastrointestinal tract; lung;
KW salivary gland; oncogene; antibody.
XX
XX Synthetic.
OS
XX US6028059-A.
PN
XX
XX 22-FEB-2000.
PD
XX
```

PF 24-JUN-1996; 96US-0668706.
XX
PR 06-SEP-1994; 94US-0301339.
XX 06-JUN-1995; 95US-0468252.
PA (UABR-) UAB RES FOUND.
XX
PI Deshane J, Curriel DT;
XX
DR WPI; 2000-316240/27.
DR N-PSDB; AAZ98748.
XX
PT Controlling neoplastic cells which over express the transmembrane
PT protein kinase receptor protein erbB2 for the treatment of cancer using
PT intracellularly expressed antibodies
XX
PS Example 1; Column 37-38; 40pp; English.
XX
CC This sequence represents the anti-erbB2 sFv amino acid sequence. The
CC nucleotide sequence is used in the method of the invention which relates
CC to killing or inhibiting a neoplastic cell expressing the oncoprotein
CC erbB2. ErbB2 is a transmembrane kinase receptor protein that stimulates
CC proliferation in a cell. The method comprises introducing into the cell,
CC a nucleic acid molecule encoding an antibody homologue e.g. anti-erbB2
CC sFv. The antibody is expressed intracellularly in the endoplasmic
CC reticulum and causes the cell to die. The method may be used for treating
CC cancers associated with over expression or amplification of the gene
CC encoding oncoprotein erbB2. ErbB2 has been found to be over expressed in
CC a variety of human epithelial carcinomas including malignancies of the
CC breast, ovary, gastrointestinal tract, salivary gland and lung. In the
CC case of ovarian and breast carcinomas, a direct correlation has been
CC found between over expression of erbB2 and aggressive tumour growth and
CC reduced patient survival. The antibody used in the method, targets
CC immature intracellular forms of erbB2 causing disruption of surface
CC expression of erbB2. The action of the antibody on cells that overexpress
CC erbB2 causes the inhibition of both cell proliferation and cell survival.
XX
SQ Sequence 237 AA;

Query Match 76.3%; Score 74; DB 21; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00048;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:|||||:|||||:
Db 171 INPYNGDTNYNQKFK 185

RESULT 13
AAE15814
ID AAE15814 standard; peptide; 17 AA.
XX
AC AAE15814;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human mAb 12B1 VH complementarity determining region (CDR) #2.
XX
KW Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;
KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;
KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;
KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;
KW immunoglobulin; complementarity determining region; CDR; protozoacide;
KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;
KW fungicide; neuroprotective; heavy chain variable region; VH; mAb;
KW monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200190193-A1.
XX
PD 29-NOV-2001.
XX

PF 24-MAY-2001; 2001WO-US16864.
XX
PR 24-MAY-2000; 2000US-0577930.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Abrahamson JA, Kikly KK;
XX
DR WPI; 2002-083094/11.
XX
PT Novel monoclonal antibody that binds to human sialoadhesin factor-3 for
PT treating or preventing cancer, inflammation, autoimmunity, allergy,
PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections
PT
XX
PS Claim 13; Page 66; 69pp; English.
XX
CC The invention relates to monoclonal antibodies that bind to human
CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or
CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central
CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple
CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections
CC and for modulating an immune response in a mammal, where the immune
CC response is downregulated or enhanced. SAF-3 antibody is useful as
CC diagnostic and therapeutic reagents, to subcharacterise cell populations
CC during haematopoietic development, to treat anaemia, as a diagnostic
CC marker to distinguish between different forms of cancer, to purge bone
CC marrow ex vivo of cancer cells expressing SAF-3, as a tool to aid in the
CC ex vivo expansion (proliferation and/or differentiation) of
CC haematopoietic progenitor cells expressing SAF-3, as a stimulus in vivo
CC for stem cell mobilisation into the periphery and as an vivo
CC chemoprotective agent. Protein comprising immunoglobulin complementarity
CC determining region (CDR) of SAF-3 antibody and its nucleic acid is
CC useful to configure screening methods for detecting the effect of added
CC compounds on the production of mRNA and polypeptide in cells.
CC The present sequence is complementarity determining region of human
CC monoclonal antibody (mAb) 12B1 heavy chain variable region (VH), which
CC binds to SAF-3.
XX
SQ Sequence 17 AA;

Query Match 73.2%; Score 71; DB 23; Length 17;
Best Local Similarity 80.0%; Pred. No. 7.7e-05;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:|||||:|||||:
Db 2 IDPYNDTGYNQKFK 16

RESULT 14
AAR27008
ID AAR27008 standard; peptide; 98 AA.
XX
AC AAR27008;
XX
DT 20-MAY-1998 (first entry)
XX
DE Hypercalcaemia agent portion 1.
XX
KW Antihuman parathyroid hormone-related protein; monoclonal antibody;
KW variable region; rodent/human chimeric MAb; constant region; PTHrP.
XX
OS Synthetic.
XX
PN JP04228089-A.
XX
PD 18-AUG-1992.
XX
PF 15-MAY-1991; 91JP-0110565.
XX
PR 15-MAY-1990; 90JP-0124581.

XX (KANF) KANEKA CORP.
PA
XX WPI; 1992-320987/39.
DR
XX
XX Treatment and preventive agent for hypercalcaemia - contg. one of
PT anti-human para-thyroid-hormone-related protein monoclonal antibody,
PT a rodent or chimera monoclonal antibody, fused gene and cell
PT line, etc.
XX
XX Disclosure; Page 13; 18pp; Japanese.
PS
XX The sequences given in AAR27008-11 are fragments which were used in
CC the construction of an agent for the treating and prevention of
CC hypercalcaemia. The agent contained a portion of the antihuman
CC parathyroid hormone-related protein monoclonal antibody (antihuman
CC pTHrp MAb). The MAb was used as the active component in the agent.
CC The agent further comprises a rodent/human chimeric MAb which has a
CC rodent variable region and a human constant region and recognises
CC human pTHrp.
XX
SQ Sequence 98 AA;

Query Match 73.2%; Score 71; DB 13; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.00055;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:||||| |
Db 43 INPYNGDTFYNQKFK 57

RESULT 15
AAR79243
ID AAR79243 standard; Protein; 108 AA.
XX
AC AAR79243;
XX
DT 21-DEC-1995 (first entry)
XX
DE Heavy chain variable region for monoclonal antibody 5G4.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW heavy chain.
XX
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
DR WPI; 1995-275415/36.
DR N-PSDB; AAQ97500.
XX
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX
PS Claim 13; Page 57; 106pp; English.
XX
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,

CC 5B6 and 3E8) were producing MABs that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
XX
SQ Sequence 108 AA;

Query Match 73.2%; Score 71; DB 16; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.00061;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:||||| |
Db 45 INPYNGDTFYNQKFK 59

Search completed: March 10, 2003, 16:56:58
Job time : 49.069 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 11.3103 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	AA44594	Mouse anti-IL-18 a
2	21	100.0	7	AA91101	Human Kiss-1 PEPTI
3	21	100.0	8	AA91099	Human Kiss-1 PEPTI
4	21	100.0	9	AA91098	Human Kiss-1 PEPTI
5	21	100.0	10	AA91097	Human Kiss-1 PEPTI
6	21	100.0	10	AAG95320	Human complementar
7	21	100.0	14	AA96847	Human peptide #122
8	21	100.0	15	AAW59970	Phosphotransferase
9	21	100.0	15	AA91096	Human Kiss-1 PEPTI
10	21	100.0	18	AAW66645	HSV-2 glycoprotein

11	21	100.0	18	19	AAW66646	HSV-2 glycoprotein
12	21	100.0	20	20	AA426958	Human/rat TrkA pro
13	21	100.0	24	19	AAW36898	Leucine rich motif
14	21	100.0	24	19	AAW36901	Leucine rich motif
15	21	100.0	25	19	AAW40518	Human TrkA leucine
16	21	100.0	25	20	AA40047	Peptide sequence d
17	21	100.0	30	19	AAW53267	Herpes simplex vir
18	21	100.0	32	20	AA12540	Human 5' EST secre
19	21	100.0	34	22	ABG21915	Novel human diagno
20	21	100.0	34	22	AAG74972	Human colon cancer
21	21	100.0	38	22	AAW99240	Human pituitary ad
22	21	100.0	38	22	AAW99241	Human pituitary ad
23	21	100.0	38	22	AAW99242	Human pituitary ad
24	21	100.0	38	22	AAW99243	Human pituitary ad
25	21	100.0	38	22	AAW99244	Human pituitary ad
26	21	100.0	38	22	AAW99245	Human pituitary ad
27	21	100.0	38	22	AAW99246	Human pituitary ad
28	21	100.0	38	22	AAW99247	Human pituitary ad
29	21	100.0	38	22	AAW99248	Human pituitary ad
30	21	100.0	38	22	AAW99249	Human pituitary ad
31	21	100.0	38	22	AAW99250	Human pituitary ad
32	21	100.0	38	22	AAW99251	Human pituitary ad
33	21	100.0	38	22	AAW99253	Human pituitary ad
34	21	100.0	38	22	AAW99255	Human pituitary ad
35	21	100.0	38	22	AAW99256	Human pituitary ad
36	21	100.0	38	22	AAW99257	Human pituitary ad
37	21	100.0	38	22	AAW99258	Human pituitary ad
38	21	100.0	38	22	AAW99259	Human pituitary ad
39	21	100.0	38	22	AAW99260	Human pituitary ad
40	21	100.0	38	22	AAW99261	Human pituitary ad
41	21	100.0	38	22	AAW99262	Human pituitary ad
42	21	100.0	38	22	AAW99263	Human pituitary ad
43	21	100.0	38	22	AAW99264	Human pituitary ad
44	21	100.0	38	22	AAW99265	Human pituitary ad
45	21	100.0	38	22	AAW99266	Human pituitary ad

ALIGNMENTS

RESULT 1

AA44594	AA44594	standard; Protein; 4 AA.
ID	AA44594	standard; Protein; 4 AA.
XX		
AC	AA44594;	
XX		
DT	04-APR-2000	(first entry)
XX		
DE	Mouse anti-IL-18 antibody VH complementarity-determining region-3.	
XX		
KW	Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;	
KW	complementarity-determining region; CDR; hybridoma #125-2H; mouse;	
KW	monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;	
KW	immunosuppressive; leucocytopenic; antialgic; antipyretic;	
KW	antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;	
KW	inflammatory disorder; immunoreaction.	
XX		
OS	Mus musculus.	
XX		
PN	EP974600-A2.	
XX		
PD	26-JAN-2000.	
XX		
PF	24-JUN-1999;	99EP-0304977.
XX		
PR	24-JUN-1998;	98JP-0177580.
PR	12-OCT-1998;	98JP-0289044.
PR	22-DEC-1998;	98JP-0365023.
XX		
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
XX		
PI	Nishida Y, Okura T, Tanimoto T, Kurimoto M;	
XX		

DR WPI; 2000-118341/11.
DR N-PSDB; AAZ49541.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
PS Claim 7; Page 19; 36pp; English.
XX
CC The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-interleukin-18 antibody heavy chain variable region
CC (VH) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2HmAb, which is capable of neutralising biological activities of
CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
CC leucocytopenetic, antialgic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. NO. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
IIII
Db 1 GLRF 4

RESULT 2
AAAY91101
ID AAY91101 standard; Peptide; 7 AA.
XX
AC AAY91101;
XX

DT 11-SEP-2000 (first entry)
XX
DE Human Kiss-1 PEPTIDE(48-54) amino acid sequence SEQ ID NO:21.
XX

KW G protein-coupled receptor protein; rOT7Tl75; hOT7Tl75; tumour;
KW guanine nucleotide binding protein; cytostatic; anti-proliferative;
KW cancer; diagnosis; Kiss-1.
XX

OS Homo sapiens.
XX
XX WO200024890-A1.
PN
XX 04-MAY-2000.
PD

XX 26-OCT-1999; 99WO-JP05905.
PF
XX 27-OCT-1998; 98JP-0305949.
PR
XX 04-FEB-1999; 99JP-0027710.
PR
XX 04-MAR-1999; 99JP-0057207.
PR
XX 29-SEP-1999; 99JP-0276225.
XX

PA (TAKE) TAKEDA CHEM IND LTD.
XX

PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
XX

DR WPI; 2000-350732/30.
DR N-PSDB; AAA39352.
XX

PT G protein coupled receptor protein, antibodies to it and a method of
PT screening compounds which alter the binding of the receptor to its
PT ligands for treatment of diseases including tumors -
XX

PS Example 3; Page 112; 114pp; Japanese.
XX

CC The present invention describes a human and a rat G protein-coupled
CC receptor protein, designated hOT7Tl75 and rOT7Tl75 respectively. The

CC G protein-coupled receptor protein has cytostatic and anti-proliferative
CC activities. The protein and antibodies raised against it are useful in
CC the diagnosis, treatment and prevention of disorders with which the
CC G protein-coupled receptor protein is associated, in particular for
CC inhibition of the proliferation of cancers such as lung, kidney, liver,
CC pancreas, colon, breast and ovary cancer. The protein is also used to
CC identify ligands to it by their ability to bind to all or part of the
CC sequence of the protein and for identifying compounds which affect the
CC binding of the protein to its ligands. The present sequence represents
CC a peptide derived from the human Kiss-1 protein, which is used in the
CC exemplification of the present invention.
XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 21; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. NO. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
IIII
Db 4 GLRF 7

RESULT 3
AAAY91099
ID AAY91099 standard; Peptide; 8 AA.
XX

AC AAY91099;
XX

DT 11-SEP-2000 (first entry)
XX

DE Human Kiss-1 PEPTIDE(47-54) amino acid sequence SEQ ID NO:14.
XX

KW G protein-coupled receptor protein; rOT7Tl75; hOT7Tl75; tumour;
KW guanine nucleotide binding protein; cytostatic; anti-proliferative;
KW cancer; diagnosis; Kiss-1.
XX

OS Homo sapiens.
XX

PN WO200024890-A1.
XX

PD 04-MAY-2000.
XX

PF 26-OCT-1999; 99WO-JP05905.
XX

PR 27-OCT-1998; 98JP-0305949.
PR

PR 04-FEB-1999; 99JP-0027710.
PR

PR 04-MAR-1999; 99JP-0057207.
PR

PR 29-SEP-1999; 99JP-0276225.
XX

PA (TAKE) TAKEDA CHEM IND LTD.
XX

PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
XX

DR WPI; 2000-350732/30.
DR N-PSDB; AAA39351.

XX
PT G protein coupled receptor protein, antibodies to it and a method of
PT screening compounds which alter the binding of the receptor to its
PT ligands for treatment of diseases including tumors -
XX

PS Claim 23; Page 109; 114pp; Japanese.
XX

CC The present invention describes a human and a rat G protein-coupled
CC receptor protein, designated hOT7Tl75 and rOT7Tl75 respectively. The
CC G protein-coupled receptor protein has cytostatic and anti-proliferative
CC activities. The protein and antibodies raised against it are useful in
CC the diagnosis, treatment and prevention of disorders with which the
CC G protein-coupled receptor protein is associated, in particular for
CC inhibition of the proliferation of cancers such as lung, kidney, liver,
CC pancreas, colon, breast and ovary cancer. The protein is also used to
CC identify ligands to it by their ability to bind to all or part of the
CC sequence of the protein and for identifying compounds which affect the

CC binding of the protein to its ligands. The present sequence represents
CC a specifically claimed peptide derived from the human Kiss-1 protein,
CC which is used in the exemplification of the present invention.

XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 21; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 5 GLRF 8

RESULT 4
AAY91098
ID AAY91098 standard; Peptide; 9 AA.
XX
AC AAY91098;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human Kiss-1 PEPTIDE(46-54) amino acid sequence SEQ ID NO:13.
XX
KW G protein-coupled receptor protein; rOT7Tl75; hOT7Tl75; tumour;
KW guanine nucleotide binding protein; cytostatic; anti-proliferative;
KW cancer; diagnosis; Kiss-1.
XX
OS Homo sapiens.
XX
PN WO200024890-A1.
XX
PD 04-MAY-2000.
XX
PF 26-OCT-1999; 99WO-JP05905.
XX
PR 27-OCT-1998; 98JP-0305949.
PR 04-FEB-1999; 99JP-0027710.
PR 04-MAR-1999; 99JP-0057207.
PR 29-SEP-1999; 99JP-0276225.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
XX
DR WPI; 2000-350732/30.
DR N-PSDB; AAA39350.
XX
PT G protein coupled receptor protein, antibodies to it and a method of
PT screening compounds which alter the binding of the receptor to its
PT ligands for treatment of diseases including tumors
XX
PS Claim 23; Page 108; 114pp; Japanese.
XX
CC The present invention describes a human and a rat G protein-coupled
CC receptor protein, designated hOT7Tl75 and rOT7Tl75 respectively. The
CC G protein-coupled receptor protein has cytostatic and anti-proliferative
CC activities. The protein and antibodies raised against it are useful in
CC the diagnosis, treatment and prevention of disorders with which the
CC G protein-coupled receptor protein is associated, in particular for
CC inhibition of the proliferation of cancers such as lung, kidney, liver,
CC pancreas, colon, breast and ovary cancer. The protein is also used to
CC identify ligands to it by their ability to bind to all or part of the
CC sequence of the protein and for identifying compounds which affect the
CC binding of the protein to its ligands. The present sequence represents
CC a specifically claimed peptide derived from the human Kiss-1 protein,
CC which is used in the exemplification of the present invention.

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 6 GLRF 9

RESULT 5
AAY91097
ID AAY91097 standard; Peptide; 10 AA.
XX
AC AAY91097;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human Kiss-1 PEPTIDE(45-54) amino acid sequence SEQ ID NO:12.
XX
KW G protein-coupled receptor protein; rOT7Tl75; hOT7Tl75; tumour;
KW guanine nucleotide binding protein; cytostatic; anti-proliferative;
KW cancer; diagnosis; Kiss-1.
XX
OS Homo sapiens.
XX
PN WO200024890-A1.
XX
PD 04-MAY-2000.
XX
PF 26-OCT-1999; 99WO-JP05905.
XX
PR 27-OCT-1998; 98JP-0305949.
PR 04-FEB-1999; 99JP-0027710.
PR 04-MAR-1999; 99JP-0057207.
PR 29-SEP-1999; 99JP-0276225.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
XX
DR WPI; 2000-350732/30.
DR N-PSDB; AAA39349.
XX
PT G protein coupled receptor protein, antibodies to it and a method of
PT screening compounds which alter the binding of the receptor to its
PT ligands for treatment of diseases including tumors
XX
PS Claim 23; Page 108; 114pp; Japanese.
XX
CC The present invention describes a human and a rat G protein-coupled
CC receptor protein, designated hOT7Tl75 and rOT7Tl75 respectively. The
CC G protein-coupled receptor protein has cytostatic and anti-proliferative
CC activities. The protein and antibodies raised against it are useful in
CC the diagnosis, treatment and prevention of disorders with which the
CC G protein-coupled receptor protein is associated, in particular for
CC inhibition of the proliferation of cancers such as lung, kidney, liver,
CC pancreas, colon, breast and ovary cancer. The protein is also used to
CC identify ligands to it by their ability to bind to all or part of the
CC sequence of the protein and for identifying compounds which affect the
CC binding of the protein to its ligands. The present sequence represents
CC a specifically claimed peptide derived from the human Kiss-1 protein,
CC which is used in the exemplification of the present invention.

XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 21; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 7 GLRF 10

RESULT 6

AAG95320
ID AAG95320 standard; Peptide; 10 AA.
XX
AC AAG95320;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 1514.
XX
KW Human; complementary peptide; ligand; drug discovery; drug design.
XX
OS Homo sapiens.
XX
PN WO200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04776.
XX
PR 13-DEC-1999; 99GB-0029464.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-408419/43.
XX
PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -
XX
PS Example 4; Page 259; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 21; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db 4 GLRF 7
RESULT 7
AAM96847
ID AAM96847 standard; Peptide; 14 AA.
XX
AC AAM96847;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #122 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX

PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Disclosure; Page 3694; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 21; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db 6 GLRF 9
RESULT 8
AAW59970
ID AAW59970 standard; peptide; 15 AA.
XX
AC AAW59970;
XX
DT 02-DEC-1998 (first entry)
XX
DE Phosphotransferase system inhibition peptide 14.
XX
KW Phosphotransferase system; PTS; inhibition; antimicrobial;
KW phage display; hydrolysis; infectious disease; respiratory infection;
KW diarrhoeal disease; tuberculosis; neonatal tetanus; whooping cough;
KW phosphohydrolase.
XX
OS Synthetic.
XX
PN EP866075-A2.
XX
XX EP866075-A2.
PD 23-SEP-1998.
XX
PF 02-FEB-1998; 98EP-0101704.
XX
PR 19-FEB-1997; 97EP-0102616.

XX (ARPI-) ARPIDA.
PA
XX
PI Erni B;
XX
DR WPI; 1998-482931/42.
XX
XX Drug target system for specific new antimicrobial agents comprises
PT uncoupling or inhibiting bacterial phosphotransferase system - used
PT to treat infections e.g. respiratory infections, diarrhoeal
PT diseases, tuberculosis and whooping cough
XX
PS Claim 8; Page 25; 25pp; English.
XX
CC This is the amino acid of a phosphotransferase system (PTS) inhibition
CC peptide identified by phage display. It is used in the method of the
CC invention as part of a drug target system for specific antimicrobials
CC comprising uncoupling or inhibition of the bacterial PTS by using a
CC phosphoryl group acceptor which is not part of the system and
CC hydrolyses spontaneously or under the influence of non-specific
CC endogenous phosphohydrolases or inhibiting the phosphotransferase
CC system actively with chemical compounds which block or inactivate at
CC least one of the enzymes of the phosphotransferase system. The
CC peptides are used to treat infectious diseases e.g. respiratory
CC infections, diarrhoeal diseases, tuberculosis, neonatal tetanus and
CC whooping cough.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 21; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db ||||
1 GLRF 4

RESULT 9
AAY91096
ID AAY91096 standard; Peptide; 15 AA.
XX
AC AAY91096;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human Kiss-1 PEPTIDE(40-54) amino acid sequence SEQ ID NO:11.
XX
KW G protein-coupled receptor protein; rOT7T175; hOT7T175; tumour;
KW guanine nucleotide binding protein; cytostatic; anti-proliferative;
KW cancer; diagnosis; Kiss-1.
XX
OS Homo sapiens.
XX
PN WO200024890-A1.
XX
PD 04-MAY-2000.
XX
PF 26-OCT-1999; 99WO-JP05905.
XX
PR 27-OCT-1998; 98JP-0305949.
PR 04-FEB-1999; 99JP-0027710.
PR 04-MAR-1999; 99JP-0057207.
PR 29-SEP-1999; 99JP-0276225.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
XX
DR WPI; 2000-350732/30.
DR N-PSDB; AAA39348.
XX
PT G protein coupled receptor protein, antibodies to it and a method of

PT screening compounds which alter the binding of the receptor to its
PT ligands for treatment of diseases including tumors
XX
PS Claim 23; Page 107-108; 114pp; Japanese.
XX
CC The present invention describes a human and a rat G protein-coupled
CC receptor protein, designated hOT7T175 and rOT7T175 respectively. The
CC G protein-coupled receptor protein has cytostatic and anti-proliferative
CC activities. The protein and antibodies raised against it are useful in
CC the diagnosis, treatment and prevention of disorders with which the
CC G protein-coupled receptor protein is associated, in particular for
CC inhibition of the proliferation of cancers such as lung, kidney, liver,
CC pancreas, colon, breast and ovary cancer. The protein is also used to
CC identify ligands to it by their ability to bind to all or part of the
CC sequence of the protein and for identifying compounds which affect the
CC binding of the protein to its ligands. The present sequence represents
CC a specifically claimed peptide derived from the human Kiss-1 protein,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 21; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db ||||
12 GLRF 15

RESULT 10
AAW66645
ID AAW66645 standard; peptide; 18 AA.
XX
AC AAW66645;
XX
DT 30-NOV-1998 (first entry)
XX
DE HSV-2 glycoprotein G partial sequence (residues 231-248).
XX
KW Herpes simplex virus type 2; HSV-2 antibody; detection; HSV-1;
KW multiply displayed peptide structure.
XX
OS Synthetic.
OS Herpes simplex virus type 2.
XX
PN GB23233360-A.
XX
PD 23-SEP-1998.
XX
PF 14-JAN-1997; 97GB-0000660.
XX
PR 14-JAN-1997; 97GB-0000660.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Marsden HS;
XX
DR WPI; 1998-459516/40.
XX
PT New peptide compounds useful for detecting herpes simplex virus type
PT 2 - can differentiate between herpes simplex virus type 1 and type 2
XX
PS Example 1; Page 10; 25pp; English.
XX
CC The invention relates to a multiply displayed peptide structure of
CC formula [(X1)p-A-(X2)q-Sp]n-Core. X1, X2 = 1-6 non-interfering amino
CC acid residues; A = Glu Glu Phe Glu Gly Ala Gly Asp Gly Glu Pro Glu
CC Asp Asp Asp; Sp = spacer group extending outwardly from the core; n at
CC least 4; and p, q = 0 or 1. The linkage between the core and the spacer
CC may be chemical or physical. Peptides of this formula are used in the
CC diagnosis of herpes simplex virus type 2 (HSV-2). The peptides can
CC distinguish HSV-2 from HSV-1. A series of 67 peptides (AAW66624-W66690),

CC mostly 18 amino acids long, that spanned amino acids 21-699 of the
CC predicted open reading frame of HSV gG2 were synthesised. The peptides
CC were made as multiply displayed peptide structures of the invention and
CC were screened against sera from HSV-1, HSV-2 antibody-positive
CC individuals and from individuals having no laboratory evidence of HSV
CC infection. From the results, peptide 55 (AAW66678) was considered a
CC likely candidate for type specific serodiagnosis of HSV.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 21; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
|
Db 15 GLRF 18

RESULT 11
AAW66646
ID AAW66646 standard; peptide; 18 AA.
XX
AC AAW66646;
XX
DT 30-NOV-1998 (first entry)
XX
DE HSV-2 glycoprotein G partial sequence (residues 241-258).
XX
KW Herpes simplex virus type 2; HSV-2 antibody; detection; HSV-1;
KW multiply displayed peptide structure.
XX
OS Synthetic.
OS Herpes simplex virus type 2.
XX
PN GB2323360-A.
XX
PD 23-SEP-1998.
XX
PF 14-JAN-1997; 97GB-0000660.
XX
PR 14-JAN-1997; 97GB-0000660.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
XX Marsden HS;
PI
XX WPI; 1998-459516/40.
DR
XX New peptide compounds useful for detecting herpes simplex virus type
PT 2 - can differentiate between herpes simplex virus type 1 and type 2
PT
XX Example 1; Page 10; 25pp; English.
PS
XX The invention relates to a multiply displayed peptide structure of
CC formula {(X1)p-A-(X2)q-Sp}n-Core. X1, X2 = 1-6 non-interfering amino
CC acid residues; A = Glu Gly Phe Glu Gly Ala Gly Asp Gly Glu Pro Glu
CC Asp Asp Asp; Sp = spacer group extending outwardly from the core; n at
CC least 4; and p, q = 0 or 1. The linkage between the core and the spacer
CC may be chemical or physical. Peptides of this formula are used in the
CC diagnosis of herpes simplex virus type 2 (HSV-2). The peptides can
CC distinguish HSV-2 from HSV-1. A series of 67 peptides (AAW66624-W66690),
CC mostly 18 amino acids long, that spanned amino acids 21-699 of the
CC predicted open reading frame of HSV gG2 were synthesised. The peptides
CC were made as multiply displayed peptide structures of the invention and
CC were screened against sera from HSV-1, HSV-2 antibody-positive
CC individuals and from individuals having no laboratory evidence of HSV
CC infection. From the results, peptide 55 (AAW66678) was considered a
CC likely candidate for type specific serodiagnosis of HSV.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 21; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
|
Db 5 GLRF 8

RESULT 12
AAY26958
ID AAY26958 standard; peptide; 20 AA.
XX
AC AAY26958;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human/rat TrkA protein fragment amino acids 99-118.
XX
KW Human; TrkA; nerve growth factor; NGF; receptor; antibody; diagnosis;
KW neurodegeneration; Alzheimer's disease; Parkinson's disease; cytoplasm;
KW Huntington's disease; amyotrophic lateral sclerosis; gangliosidosis;
KW nuclear translocation.
XX
OS Homo sapiens.
OS Rattus sp.
XX
PN WO9948908-A2.
XX
PD 30-SEP-1999.
XX
PF 26-MAR-1999; 99WO-FR00716.
XX
PR 26-MAR-1998; 98FR-0004011.
XX
PA (CNRS) CENT NAT RECH SCI.
XX
PI Rudkin B;
XX
DR WPI; 1999-572168/48.
XX
PT New fragments of the TrkA receptor for nerve growth factor, for
PT diagnosis, prevention and treatment of neurodegeneration -
XX
PS Claim 5; Page 14; 15pp; French.
XX
CC The invention relates to the use of a TrkA protein (the nerve growth
CC factor (NGF) receptor (AAY26956)) or fragments (AAY26957-Y26963) of TrkA
CC to raise antibodies to the TrkA polypeptide. The fragments especially
CC cover amino acids (aa) 71-87, 125-141, 265-283, 379-392 or 382-417. The
CC protein or fragments, also the 99-118 aa fragment of TrkA, and their
CC related antibodies and nucleic acids are used for diagnosis, prevention
CC and treatment of neurodegeneration, e.g. Alzheimer's, Parkinson's and
CC Huntington's diseases, amyotrophic lateral sclerosis and GM1
CC gangliosidosis, associated with abnormal regulation of TrkA. The protein
CC can be used to raise specific antibodies and these used to determine
CC cellular localization of TrkA and to provide information on the form of
CC the receptor (and thus of NGF activity). Especially after
CC internalization of TrkA, induced by NGF, only the extracellular receptor
CC domain undergoes nuclear translocation, with the intracellular domain
CC retained in the cytoplasm.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 21; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
|
Db 4 GLRF 7

RESULT 13

AAW36898
ID AAW36898 standard; peptide; 24 AA.
XX
AC AAW36898;
XX
DT 01-APR-1998 (first entry)
XX
DE Leucine rich motif peptide of the human tyrosine kinase receptor A.
XX
KW Leucine rich motif; LRM2; extracellular domain;
KW tyrosine kinase receptor A; neurotrophin binding region;
KW neurotrophin activity agonist; neurotrophin activity antagonist.
XX
OS Homo sapiens.
XX
PN US5688911-A.
XX
PD 18-NOV-1997.
XX
PF 03-MAY-1995; 95US-0434198.
XX
PR 03-MAY-1995; 95US-0434198.
XX
PA (SCHN/) SCHNEIDER R.
PA (WIND/) WINDISCH J M.
XX
PI Schneider R, Windisch JM;
XX
DR WPI; 1998-008037/01.
XX
PT Tyrosine kinase receptor peptide(s) - useful in screening assays for
PT neurotrophin agonists and antagonists
XX
PS Claim 1; Column 13; 8pp; English.
XX
CC The present sequence represents a novel leucine rich motif (LRM2)
CC derived from the extracellular domains of the human tyrosine kinase
CC receptor A. The peptide constitutes the neurotrophin binding region
CC of the receptor. The peptide may be used as an agonist of neurotrophin
CC activity, or may be used in screening assays to identify compounds
CC capable of binding the region critical to neurotrophin/tyrosine kinase
CC receptor interaction, thereby acting as either antagonists or agonists
CC of neurotrophin activity.
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 21; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db ||||
6 GLRF 9
RESULT 14
AAW36901
ID AAW36901 standard; peptide; 24 AA.
XX
AC AAW36901;
XX
DT 01-APR-1998 (first entry)
XX
DE Leucine rich motif peptide of the rat tyrosine kinase receptor A.
XX
KW Leucine rich motif; LRM2; extracellular domain;
KW tyrosine kinase receptor A; neurotrophin binding region;
KW neurotrophin activity agonist; neurotrophin activity antagonist.
XX
OS Rattus sp.
XX
PN US5688911-A.
XX

18-NOV-1997.
XX
PF 03-MAY-1995; 95US-0434198.
XX
PR 03-MAY-1995; 95US-0434198.
XX
PA (SCHN/) SCHNEIDER R.
PA (WIND/) WINDISCH J M.
XX
PI Schneider R, Windisch JM;
XX
DR WPI; 1998-008037/01.
XX
PT Tyrosine kinase receptor peptide(s) - useful in screening assays for
PT neurotrophin agonists and antagonists
XX
PS Claim 1; Column 13; 8pp; English.
XX
CC The present sequence represents a novel leucine rich motif (LRM2)
CC derived from the extracellular domains of the rat tyrosine kinase
CC receptor A. The peptide constitutes the neurotrophin binding region
CC of the receptor. The peptide may be used as an agonist of neurotrophin
CC activity, or may be used in screening assays to identify compounds
CC capable of binding the region critical to neurotrophin/tyrosine kinase
CC receptor interaction, thereby acting as either antagonists or agonists
CC of neurotrophin activity.
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 21; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db ||||
6 GLRF 9
RESULT 15
AAW40518
ID AAW40518 standard; protein; 25 AA.
XX
AC AAW40518;
XX
DT 15-JUL-1998 (first entry)
XX
DE Human TrkA leucine rich motif LRM-2A fragment.
XX
KW Nerve growth factor; NGF; optical structure; active conformation;
KW variable basis Monte Carlo stimulated annealing; VBMC; ligand;
KW neurotrophin; agonist; inhibitor; TrkA; TrkB; TrkC; NT3; p75NTR;
KW brain-derived neurotrophic factor; human.
XX
OS Homo sapiens.
XX
PN WO9806048-A2.
XX
PD 12-FEB-1998.
XX
PF 31-JUL-1997; 97WO-CA00539.
XX
PR 31-JUL-1996; 96GB-0016105.
XX
PA (TOOH) UNIV QUEENS KINGSTON.
XX
PI Riopelle RJ, Ross GM, Shamovsky IL, Weaver DF;
XX
DR WPI; 1998-145797/13.
XX
PT Identifying optimal molecular structures by variable basis Monte
PT Carlo method - particularly to determine biologically active
PT conformation(s) of neurotrophin domains involved in receptor binding
PT and subsequent evolution of active ligands

xx Disclosure; Fig 14; 170pp; English.
PS
xx
CC Protein fragments AAW40504-W40523 are used in a variable basis Monte
CC Carlo (VPMC) stimulated annealing method for identifying an optimal
CC molecular structure. The method is used to identify the biologically
CC active conformations of peptide domains of ligands, particularly
CC neurotrophins (NT), that bind to a receptor. Once such conformations have
CC been identified, small molecules that either inhibit NT-binding or act
CC as agonists of the native ligand can be developed. Specifically the
CC method is applied to (a) nerve growth factor/TrkA; (b) brain-derived
CC neurotrophic factor, NT3 or 4/TrkB; (c) NT3/TrkC and (d) the receptor
CC p75NTR. The preferred ligand comprises elements with proper spatial
CC occupancy, relative atomic positions, bond type and charge for defining
CC a 3-dimensional configuration able to bind the 3 binding areas. TrkA
CC includes a leucine-rich motif (LRM), amino acids 93-117, with 5 binding
CC areas: (A) Phe105TA (hydrophobic interaction); (B) Phe111TA, Phe113TA
CC and Thr114TA (hydrophobic interaction); (C) Asn109TA and His112TA
CC (ionic); (D) Lys100TA (ionic) and (E) Asn95TA-Ile98TA (multiple parallel
CC beta -strand type hydrogen bonds).
xx
SQ Sequence 25 AA;

Query Match 100.0%; Score 21; DB 19; Length 25;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
' ||||
Db 10 GLRF 13

Search completed: March 10, 2003, 16:56:58
Job time : 11.3103 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 22.069 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	46	79.3	489	11	Q8VCX4	Q8vcx4 mus musculu
2	45	77.6	473	11	Q9D8L4	Q9d8l4 mus musculu
3	43	74.1	481	11	Q8VCV5	Q8vcv5 mus musculu
4	42	72.4	117	11	Q9QXF0	Q9qxf0 mus musculu
5	42	72.4	117	11	Q9QXE9	Q9qxe9 mus musculu
6	42	72.4	586	10	Q9SNT3	Q9snt3 oryza sativ
7	41	70.7	253	16	Q8X4Z9	Q8x4z9 escherichia
8	41	70.7	310	8	Q63625	Q63625 dalbulus eb
9	41	70.7	310	8	Q63635	Q63635 baldulus tr
10	41	70.7	310	8	Q63636	Q63636 baldulus tr
11	41	70.7	481	11	Q91W11	Q91wt1 mus musculu
12	41	70.7	550	2	O50266	O50266 agrobacteri
13	40	69.0	275	4	Q96LU7	Q96lu7 homo sapien
14	40	69.0	310	8	Q63624	Q63624 dalbulus ci
15	40	69.0	310	8	Q63626	Q63626 dalbulus el
16	40	69.0	310	8	Q63629	Q63629 dalbulus gu

17	40	69.0	310	8	O63630	O63630 dalbulus lo
18	40	69.0	372	10	P93103	P93103 chenopodium
19	40	69.0	481	11	Q91WT3	Q91wt3 mus musculu
20	40	69.0	969	17	O28863	O28863 archaeoglob
21	39	67.2	102	11	Q9JL79	Q9jl79 mus musculu
22	39	67.2	114	11	Q9JL81	Q9jl81 mus musculu
23	39	67.2	117	11	Q9Z1C6	Q9z1c6 mus musculu
24	39	67.2	142	10	Q8W018	Q8w018 antirrhinum
25	39	67.2	142	10	Q8W017	Q8w017 antirrhinum
26	39	67.2	170	11	Q925S2	Q925s2 mus musculu
27	39	67.2	260	10	Q9AXC0	Q9axc0 antirrhinum
28	39	67.2	283	8	O47571	O47571 onchocerca
29	39	67.2	310	8	O63627	O63627 dalbulus ge
30	39	67.2	310	8	O63628	O63628 dalbulus ge
31	39	67.2	310	8	O63631	O63631 dalbulus ma
32	39	67.2	310	8	O63632	O63632 dalbulus ma
33	39	67.2	310	8	O63633	O63633 dalbulus ma
34	39	67.2	325	16	Q99S16	Q99s16 staphylococ
35	39	67.2	484	11	Q99LA6	Q99la6 mus musculu
36	38	65.5	157	4	O95978	O95978 homo sapien
37	38	65.5	187	2	Q8RM55	Q8rm55 bacteroides
38	38	65.5	241	11	Q921A6	Q921a6 mus musculu
39	38	65.5	310	8	O63623	O63623 dalbulus ch
40	38	65.5	339	10	Q9LJA9	Q9lja9 arabidopsis
41	38	65.5	421	16	Q97G76	Q97g76 clostridium
42	38	65.5	434	11	Q9D3S9	Q9d3s9 mus musculu
43	38	65.5	469	11	Q8R3V9	Q8r3v9 mus musculu
44	38	65.5	488	11	Q91WR1	Q91wr1 mus musculu
45	37	63.8	119	4	Q9UL94	Q9ul94 homo sapien

ALIGNMENTS

RESULT 1
Q8VCX4
ID Q8VCX4 PRELIMINARY; PRT; 489 AA.
AC Q8VCX4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 53.2 kDa protein.
GN AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322; AAH18322.1; -
DR MGI; MGI:2144917; AI893585.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;

Query Match 79.3%; Score 46; DB 11; Length 489;
Best Local Similarity 70.0%; Pred. No. 6.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTDYFIY 10
Db 45 GYTFSDYFIH 54

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018455; AAH18455.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 74.1%; Score 43; DB 11; Length 481;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 45 GYSFIDYNIY 54

RESULT 4
Q9QXF0
ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 72.4%; Score 42; DB 11; Length 117;
Best Local Similarity 66.7%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
Db 26 GYTFDYIM 34

RESULT 5
Q9QXE9
ID Q9QXE9 PRELIMINARY; PRT; 117 AA.
AC Q9QXE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
```

```

RESULT 2
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1810060O09rik protein.
GN IGH-1 OR 181006O009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 77.6%; Score 45; DB 11; Length 473;
Best Local Similarity 77.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
Db 45 GYTFDYI 53

RESULT 3
Q8VCV5
ID Q8VCV5 PRELIMINARY; PRT; 481 AA.
AC Q8VCV5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
```



```
AI2015
hypothetical protein asl1679 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AI2015
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2015
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB78045.1; PID:g17135499; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl1679

Query Match      100.0%; Score 21; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLRF 4
      ||||
Db      41 GLRF 44

RESULT 13
QOEC2
hypothetical protein A-87 - Escherichia coli plasmid pBR322
C;Species: Escherichia coli
C;Date: 31-Dec-1980 #sequence_revision 15-Oct-1982 #text_change 10-Sep-1999
C;Accession: A04479
R;Sutcliffe, J.G.
Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A;Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.
A;Reference number: A90923; MUID:80002802; PMID:383387
A;Accession: A04479
A;Molecule type: DNA
A;Residues: 1-87 <SUT>
C;Genetics:
A;Genome: plasmid
A;Start codon: GTG
C;Superfamily: Escherichia coli plasmid pBR322 hypothetical 10K protein

Query Match      100.0%; Score 21; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLRF 4
      ||||
Db      18 GLRF 21

RESULT 14
A83643
hypothetical protein PA0012 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83643
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83643
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <STO>
A;Cross-references: GB:AE004441; GB:AE004091; NID:g9945828; PIDN:AAG03402.1; GSPDB:GN001
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```
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0012

Query Match      100.0%; Score 21; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLRF 4
      ||||
Db      81 GLRF 84

RESULT 15
B84312
hypothetical protein Vng1590h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84312
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: B84312
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <STO>
A;Cross-references: GB:AE004437; NID:gl0581072; PIDN:AAG19862.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1590H

Query Match      100.0%; Score 21; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLRF 4
      ||||
Db      10 GLRF 13

Search completed: March 10, 2003, 17:01:26
Job time : 6.34483 secs
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RESULT 7
F90697
hypothetical protein ECs0550 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: F90697
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90697
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33973.1; PID:g13360008; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs0550

Query Match 100.0%; Score 21; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|||||
Db 23 GLRF 26

RESULT 8
A69010
hypothetical protein MTH1077 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: A69010
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A69010
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-75 <MTH>
A;Cross-references: GB:AE000879; GB:AE000666; NID:g2622175; PIDN:AAB85566.1; PID:g262217
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1077
A;Start codon: TTG

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|||||
Db 26 GLRF 29

RESULT 9
C36817
ORF 2 protein - human papillomavirus type 41
C;Species: human papillomavirus type 41
A;Note: host Homo sapiens (man)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 08-Oct-1999
C;Accession: C36817
R;Hirt, L.; Hirsch-Behnam, A.; De Villiers, E.M.
Virus Res. 18, 179-190, 1990
A;Title: Nucleotide sequence of human papillomavirus (HPV) type 41: an unusual HPV type
A;Reference number: A43550
A;Accession: C36817
A;Status: translation not shown

A;Molecule type: DNA
A;Residues: 1-76 <HIR>
A;Cross-references: EMBL:X56147; NID:g60942; PIDN:CAA39622.1; PID:g60953

Query Match 100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|||||
Db 68 GLRF 71

RESULT 10
T09045
hypothetical protein F26K10.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C;Accession: T09045
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Ban
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
A;Accession: T09045
A;Molecule type: DNA
A;Residues: 1-80 <BEV>
A;Cross-references: EMBL:AL049803; GSPDB:GN00062; ATSP:F26K10.170
A;Experimental source: cultivar Columbia; BAC clone F26K10
C;Genetics:
A;Gene: ATSP:F26K10.170
A;Map position: 4
A;Introns: 41/3

Query Match 100.0%; Score 21; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|||||
Db 68 GLRF 71

RESULT 11
H81188
hypothetical protein NMB0518 [imported] - Neisseria meningitidis (strain MC58 serogro
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: H81188
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81188
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <TET>
A;Cross-references: GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF40950.1; PID:g722
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0518

Query Match 100.0%; Score 21; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|||||
Db 21 GLRF 24

RESULT 12

S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0880
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-39 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02943.1; PID:g16504193; GSPDB:GN00176
C;Genetics:
A;Gene: STY3277

Query Match 100.0%; Score 21; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 5 GLRF 8

RESULT 3
D83610
hypothetical protein PA0284 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83610
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83610

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <STO>
A;Cross-references: GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AAG03673.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0284

Query Match 100.0%; Score 21; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 26 GLRF 29

RESULT 4
F75371
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75371
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75371
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <WHI>
A;Cross-references: GB:AE002007; GB:AE000513; NID:g6459402; PIDN:AAF11201.1; PID:g645940
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1640
A;Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 8 GLRF 11

RESULT 5
E96504
protein F9Cl6.27 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96504
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96504
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <STO>
A;Cross-references: GB:AE005173; NID:g8778662; PIDN:AAF79670.1; GSPDB:GN00141
C;Genetics:
A;Gene: F9Cl6.27
A;Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 38 GLRF 41

RESULT 6
PX0076
acrosin-like proteinase (EC 3.4.21.-) - pig (fragments)
N;Alternate names: cetyltrimethylammonium bromide-extracted sperm protease
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Apr-1995 #sequence_revision 24-Oct-1997 #text_change 07-May-1999
C;Accession: PX0076
R;Akama, K.; Terao, K.; Tanaka, Y.; Noguchi, A.; Yonezawa, N.; Nakano, M.; Tobita, T.
J. Biochem. 116, 464-470, 1994
A;Title: Purification and characterization of a novel acrosin-like enzyme from boar c
A;Reference number: PX0076; MUID:95122480; PMID:7822268
A;Accession: PX0076
A;Molecule type: protein
A;Residues: 1-73 <AKA>
A;Experimental source: epididymis; sperm
A;Note: this enzyme was reported to differ from acrosin in acid solubility, kinetic p
C;Superfamily: acrosin; trypsin homology
C;Keywords: epididymis; glycoprotein; hydrolase; serine proteinase; sperm

Query Match 100.0%; Score 21; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
||||
Db 11 GLRF 14

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 4.34483 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	37	2 D82636	hypothetical prote
2	21	100.0	39	2 AG0880	hypothetical prote
3	21	100.0	60	2 D83610	hypothetical prote
4	21	100.0	63	2 F75371	hypothetical prote
5	21	100.0	71	2 E96504	protein F9C16.27 [
6	21	100.0	73	2 PX0076	acrosin-like prote
7	21	100.0	73	2 F90697	hypothetical prote
8	21	100.0	75	2 A69010	hypothetical prote
9	21	100.0	76	2 C36817	ORF 2 protein - hu
10	21	100.0	80	2 T09045	hypothetical prote
11	21	100.0	83	2 H81188	hypothetical prote
12	21	100.0	84	2 AI2015	hypothetical prote
13	21	100.0	87	1 QQEC2	hypothetical prote
14	21	100.0	88	2 A83643	hypothetical prote
15	21	100.0	89	2 B84312	hypothetical prote
16	21	100.0	91	2 T17877	hypothetical prote
17	21	100.0	91	2 G97130	hypothetical prote
18	21	100.0	91	2 G97870	O-linked GlcNAc tr
19	21	100.0	93	2 T51189	small zinc finger-
20	21	100.0	94	2 AB1084	hypothetical prote
21	21	100.0	95	2 AC1903	hypothetical prote
22	21	100.0	101	2 AC0099	probable lipoprote
23	21	100.0	107	2 T35634	hypothetical prote
24	21	100.0	108	2 AD1986	hypothetical prote
25	21	100.0	110	2 G70791	hypothetical prote
26	21	100.0	112	2 E82540	conserved hypothet
27	21	100.0	112	2 G70855	hypothetical prote
28	21	100.0	115	2 AC2020	hypothetical prote
29	21	100.0	119	2 JN0295	Ig heavy chain V-D

30	21	100.0	121	2 A87307	hypothetical prote
31	21	100.0	122	2 D72128	hypothetical prote
32	21	100.0	122	2 G86494	hypothetical prote
33	21	100.0	122	2 A81543	hypothetical prote
34	21	100.0	122	2 T35702	hypothetical prote
35	21	100.0	123	2 F64342	hypothetical prote
36	21	100.0	125	2 AI1358	protein gp30 [Bact
37	21	100.0	127	1 VXCSE	preprotein translo
38	21	100.0	127	2 S50213	ubiquinol-cytochro
39	21	100.0	127	2 H91241	preprotein translo
40	21	100.0	127	2 E86089	preprotein translo
41	21	100.0	127	2 AI0456	preprotein translo
42	21	100.0	127	2 AC0934	preprotein translo
43	21	100.0	129	2 S50142	histone H3 - Leish
44	21	100.0	129	2 D90367	hypothetical prote
45	21	100.0	129	2 F82515	conserved hypothet

ALIGNMENTS

RESULT 1

D82636
hypothetical protein XF1790 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82636
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82636
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-37 <SIM>
A:Cross-references: GB:AE004001; GB:AE003849; NID:g9106864; PIDN:AAF84598.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
A:Genetics:
A:Gene: XF1790

Query Match 100.0%; Score 21; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
|
Db 3 GLRF 6

RESULT 2

AG0880

hypothetical protein STY3277 [imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0880
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr


```
RESULT 8
MHMSJ5
Ig heavy chain V region (J558) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Mar-2000
C:Accession: A26242
R:Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
Nature 283, 35-40, 1980
A:Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
A:Reference number: A26242; MUID:80078170; PMID:6765983
A:Accession: A26242
A:Molecule type: protein
A:Residues: 1-117 <SCH>
A:Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that s
C:Comment: This protein binds dextran.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; hybridoma; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:22-96/Disulfide bonds: #status predicted

Query Match          69.1%; Score 67; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0011;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
   ||:| || |||||:
Db 50 DINPNNGGTSYNQKFK 65

RESULT 9
MHMS38
Ig heavy chain V region (AC38 205.12) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 30-May-1997
C:Accession: A02040
R:Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 517-523, 1984
A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes
A:Reference number: A91000; MUID:84182519; PMID:6201362
A:Accession: A02040
A:Molecule type: protein
A:Residues: 1-118 <DIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-98/Region: V segment
F:15-98/Domain: immunoglobulin homology <IMM>
F:99-104/Region: D segment
F:105-118/Region: J segment
F:22-96/Disulfide bonds: #status predicted

Query Match          69.1%; Score 67; DB 1; Length 118;
Best Local Similarity 75.0%; Pred. No. 0.0011;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
   ||:| || |||||:
Db 50 DINPNNGGTSYNQKFK 65

RESULT 10
T01407
Ig heavy chain (myeloma M104E) - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T01407
R:Takahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamoto
Microbiol. Immunol. 36, 855-863, 1992
A:Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and
A:Reference number: Z14317; MUID:93116638; PMID:1474935
A:Accession: T01407
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
```

```
A:Residues: 1-140 <TAK>
A:Cross-references: EMBL:S51851; NID:g262657
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match          69.1%; Score 67; DB 2; Length 140;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
   ||:| || |||||:
Db 69 DINPNNGGTSYNQKFK 84

RESULT 11
A49982
Ig heavy chain V region (BA7.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: A49982
R:Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman,
J. Biol. Chem. 269, 2805-2813, 1994
A:Title: Topology of an amiloride-binding protein.
A:Reference number: A49982; MUID:94132051; PMID:8300613
A:Accession: A49982
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <LIN>
A:Cross-references: GB:L24802; NID:g452096; PIDN:AAA98740.1; PID:g452097
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          68.0%; Score 66; DB 2; Length 120;
Best Local Similarity 68.8%; Pred. No. 0.0016;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFRD 17
   | |||| |:|| |:|
Db 51 ISPYNGATTYNQNFKD 66

RESULT 12
B47159
Ig heavy chain V region, anti-carcinoembryonic maId T84.66 antigen monoclonal anti-id
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C:Accession: B47159
R:Gaida, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A:Title: Molecular characterization of a cloned idiotypic cascade containing a networ
A:Reference number: A47159; MUID:93300804; PMID:7686150
A:Accession: B47159
A>Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-136 <GAI>
A:Experimental source: hybridoma 6G6.C4
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBIP:134422)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match          68.0%; Score 66; DB 2; Length 136;
Best Local Similarity 75.0%; Pred. No. 0.0019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFRD 17
   ||||: | |||||
Db 70 IDPYDSVTHYNQKFRD 85

RESULT 13
C37263
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 18.4655 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	71	73.2	98	2 S17604	Ig heavy chain V r
2	71	73.2	114	2 S26319	Ig heavy chain V r
3	71	73.2	135	2 PS0057	Ig heavy chain pre
4	70	72.2	107	2 S26320	Ig heavy chain V r
5	70	72.2	120	2 E45722	anti-glycoprotein
6	68	70.1	106	2 S26315	Ig heavy chain V r
7	67	69.1	117	1 MHMS4E	Ig heavy chain V r
8	67	69.1	117	1 MHMSJ5	Ig heavy chain V r
9	67	69.1	118	1 MHMS38	Ig heavy chain V r
10	67	69.1	140	2 T01407	Ig heavy chain (my
11	66	68.0	120	2 A49982	Ig heavy chain V r
12	66	68.0	136	2 B47159	Ig heavy chain V r
13	65	67.0	72	2 C37263	Ig heavy chain V r
14	65	67.0	102	2 B37263	Ig heavy chain V r
15	65	67.0	113	2 S55535	Ig heavy chain V r
16	64	66.0	101	2 H37262	Ig heavy chain V r
17	64	66.0	107	2 PH0971	Ig heavy chain V r
18	64	66.0	137	2 H32513	Ig heavy chain pre
19	64	66.0	138	2 S45249	Ig heavy chain pre
20	63	64.9	93	2 S42182	Ig gamma chain V r
21	63	64.9	94	2 S42177	Ig gamma chain V r
22	63	64.9	95	2 S42178	Ig gamma chain V r
23	63	64.9	97	2 S42181	Ig gamma chain V r
24	63	64.9	101	2 S42179	Ig gamma chain V r
25	63	64.9	101	2 S42184	Ig gamma chain V r
26	63	64.9	102	2 S42180	Ig gamma chain V r
27	63	64.9	119	2 F30502	Ig heavy chain V r
28	63	64.9	136	1 HVMSB1	Ig heavy chain pre
29	62	63.9	117	1 HVMS8A	Ig heavy chain pre

ALIGNMENTS

RESULT 1
S17604
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17604
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17604
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-98 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 71; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:|||||
Db 44 INPYNGDTFYNQKFK 58

RESULT 2
S26319
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26319
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a proteol
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26319
A:Molecule type: mRNA
A:Residues: 1-114 <STA>
A:Cross-references: EMBL:X59172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 71; DB 2; Length 114;
Best Local Similarity 80.0%; Pred. No. 0.00024;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:|||||
Db 47 INPYNGDTFYNQKFK 61

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0245
A;Molecule type: mRNA
A;Residues: 1-112 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;8-91/Domain: immunoglobulin homology <IMM>
F;24-28/Region: complementarity-determining 1
F;29-42/Region: framework 2
F;43-59/Region: complementarity-determining 2
F;60-91/Region: framework 3
F;92-102/Region: complementarity-determining 3
F;103-112/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 112;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
||:||||:|
Db 19 GYTFTDYI 27

RESULT 13
S03305

Ig heavy chain V region (6B12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: J10044; S05276; S03305
R;Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A;Title: Do antibodies recognize amino acid side chains of protein antigens independentl
A;Reference number: J10043; MUID:88258372; PMID:2455014

A;Accession: J10044
A;Molecule type: mRNA
A;Residues: 1-117 <VAN>
A;Cross-references: EMBL:X12381
R;Metzger, D.W.
submitted to the EMBL Data Library, July 1988

A;Reference number: S05276
A;Accession: S05276
A;Molecule type: mRNA
A;Residues: 1-116,'T' <MET>
A;Cross-references: EMBL:X12381; NID:g52094; PIDN:CAA30939.1; PID:g930170
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 117;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
||:||||:|
Db 26 GYTFTDYI 34

RESULT 14
S37483

Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253

C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 469;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
||:||||:|
Db 45 GYTFTDYI 53

RESULT 15
S46465

Ig heavy chain V region (DA-1) - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S46465
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.;
Nature Genet. 7, 162-168, 1994

A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the te
A;Reference number: S46460; MUID:95004581; PMID:7920635
A;Accession: S46465
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <COO>

A;Cross-references: EMBL:Z29977; NID:g505454; PIDN:CAA82867.1; PID:g1335176
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 75.9%; Score 44; DB 2; Length 77;
Best Local Similarity 60.0%; Pred. No. 1.2;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
||:||||:::
Db 14 GYTFTDYMH 23

Search completed: March 10, 2003, 17:01:24
Job time : 10.8621 secs

A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Region: framework 1
F;3-86/Domain: immunoglobulin homology <IMM>
F;19-23/Region: complementarity-determining 1
F;24-37/Region: framework 2
F;38-54/Region: complementarity-determining 2
F;55-86/Region: framework 3
F;87-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:||||:|
Db 14 GYTFTDYI 22

RESULT 8
PH0999

Ig heavy chain V region (clone 74-cl) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH0999
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0999

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:||||:|
Db 25 GYTFTDYI 33

RESULT 9
PH0997

Ig heavy chain V region (clone 17s-c2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH0997
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0997

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-109 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 109;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9

Db 26 GYTFTDYI 34
||:||||:|

RESULT 10
PL0244

Ig heavy chain V region (anti-DNA, DP9VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0244
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0244

A;Molecule type: mRNA
A;Residues: 1-110 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;8-91/Domain: immunoglobulin homology <IMM>
F;24-28/Region: complementarity-determining 1
F;29-42/Region: framework 2
F;43-59/Region: complementarity-determining 2
F;60-91/Region: framework 3
F;92-102/Region: complementarity-determining 3
F;103-110/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 110;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:||||:|
Db 19 GYTFTDYI 27

RESULT 11
PH0998

Ig heavy chain V region (clone 165.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH0998
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0998

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-111 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 111;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:||||:|
Db 26 GYTFTDYI 34

RESULT 12
PL0245

Ig heavy chain V region (anti-DNA, DP17VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0245
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 81.0%; Score 47; DB 2; Length 446;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
||:||||:|
Db 26 GYTFTDYIHH 35

RESULT 3

PL0242
Ig heavy chain V region (anti-DNA, S54VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0242
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0242
A;Molecule type: mRNA
A;Residues: 1-91 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-8/Region: framework 1
F;9-13/Region: complementarity-determining 1
F;14-27/Region: framework 2
F;28-44/Region: complementarity-determining 2
F;45-76/Region: framework 3
F;77-87/Region: complementarity-determining 3
F;88-91/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 91;
Best Local Similarity 77.8%; Pred. No. 0.96;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
||:||||:|
Db 4 GYTFTDYI 12

RESULT 4

PH1165
Ig heavy chain V region (clone 26F.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1165
R;Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A;Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A;Reference number: PH1105; MUID:92364545; PMID:1500855
A;Accession: PH1165
A;Molecule type: DNA
A;Residues: 1-96 <SCH>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-96/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 96;
Best Local Similarity 77.8%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
||:||||:|
Db 26 GYTFTDYI 34

RESULT 5

H47624
Ig heavy chain V-IX region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: H47624
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variat
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: H47624
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-98 <HAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
||:||||:|
Db 26 GYTFTDYIHH 35

RESULT 6

PL0240
Ig heavy chain V region (anti-DNA, S57VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0240
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0240
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Region: framework 1
F;3-86/Domain: immunoglobulin homology <IMM>
F;19-23/Region: complementarity-determining 1
F;24-37/Region: framework 2
F;38-54/Region: complementarity-determining 2
F;55-86/Region: framework 3
F;87-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
||:||||:|
Db 14 GYTFTDYI 22

RESULT 7

PL0243
Ig heavy chain V region (anti-DNA, S7VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0243
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0243
A;Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 10.8621 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	47	81.0	246	2 S38950	Ig gamma chain - m
2	47	81.0	446	2 S40295	Ig gamma-2a chain
3	45	77.6	91	2 PL0242	Ig heavy chain V r
4	45	77.6	96	2 PH1165	Ig heavy chain V r
5	45	77.6	98	2 H47624	Ig heavy chain V-I
6	45	77.6	107	2 PL0240	Ig heavy chain V r
7	45	77.6	107	2 PL0243	Ig heavy chain V r
8	45	77.6	107	2 PH0999	Ig heavy chain V r
9	45	77.6	109	2 PH0997	Ig heavy chain V r
10	45	77.6	110	2 PL0244	Ig heavy chain V r
11	45	77.6	111	2 PH0998	Ig heavy chain V r
12	45	77.6	112	2 PL0245	Ig heavy chain V r
13	45	77.6	117	2 S03305	Ig heavy chain V r
14	45	77.6	469	2 S37483	Ig heavy chain V r
15	44	75.9	77	2 S46465	Ig gamma-2a chain
16	44	75.9	98	2 S26909	Ig heavy chain V r
17	44	75.9	110	2 PH1000	Ig heavy chain V r
18	44	75.9	288	2 S29690	Ig heavy chain VDJ
19	43	74.1	56	2 S36386	Ig heavy chain V r
20	43	74.1	101	2 S26314	Ig heavy chain V r
21	43	74.1	105	2 S67941	Ig heavy chain var
22	43	74.1	107	2 PL0241	Ig heavy chain V r
23	43	74.1	120	2 A49982	Ig heavy chain V r
24	42	72.4	102	2 PH1235	Ig heavy chain V r
25	42	72.4	106	2 PH1002	Ig heavy chain V r
26	42	72.4	108	2 PH0977	Ig heavy chain V r
27	42	72.4	108	2 PH0975	Ig heavy chain V r
28	42	72.4	109	2 PH0973	Ig heavy chain V r
29	42	72.4	109	2 PH1001	Ig heavy chain V r

30	42	72.4	112	2 S09957	Ig heavy chain V-D
31	42	72.4	113	2 PH0974	Ig heavy chain V r
32	42	72.4	117	1 MHMS4E	Ig heavy chain V r
33	42	72.4	117	1 MHMSJ5	Ig heavy chain V r
34	42	72.4	117	2 S09960	Ig heavy chain V-D
35	42	72.4	118	1 MHMS38	Ig heavy chain V r
36	42	72.4	120	2 S19963	Ig heavy chain V r
37	42	72.4	126	2 S16280	Ig heavy chain (38
38	42	72.4	139	2 PH1225	Ig heavy chain pre
39	42	72.4	140	2 T01407	Ig heavy chain (my
40	41	70.7	36	2 S33401	Ig heavy chain V r
41	41	70.7	98	1 HVMS96	Ig heavy chain V r
42	41	70.7	98	2 S26910	Ig heavy chain V r
43	41	70.7	98	2 S17604	Ig heavy chain V r
44	41	70.7	104	2 S26466	Ig heavy chain V r
45	41	70.7	114	2 S26319	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S38950

Ig gamma chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C;Accession: S38950

R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;

Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp

A;Reference number: S38950; MUID:94128242; PMID:8297501

A;Accession: S38950

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-246 <KLE>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;137-201/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.0%; Score 47; DB 2; Length 246;

Matches 7; Conservative 70.0%; Pred. No. 1.1;

Mismatches 3; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10

Db 26 GYTFTDYIYH 35

RESULT 2

S40295

Ig gamma-2a chain (mAb735) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999

C;Accession: S40295

R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;

submitted to the EMBL Data Library, January 1993

A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A;Reference number: S40295

A;Accession: S40295

A;Molecule type: protein

A;Residues: 1-446 <KLE>

C;Genetics:

A;Map position: 12

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F;1-117/Domain: V-D-J region <VDJ>

F;118-446/Domain: C region <CHR>

F;118-214/Domain: C1 region <CH1>

F;215-230/Region: hinge

F;231-340/Domain: C2 region <CH2>

F;341-446/Domain: C3 region <CH3>

F;360-427/Domain: immunoglobulin homology <IMM>

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OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=20165948; PubMed=10701121;
RA Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
RA Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,
RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
RA Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,
RA St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,
RA Ragan M.A., Sensen C.W.;
RT "Gene content and organization of a 281-kbp contig from the genome of
RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
RL Genome 43:116-136(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -!- CATALYTIC ACTIVITY: (S)-dihydrooorotate + H(2)O = N-carbamoyl-L-
CC aspartate.
CC -!- COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH
CC IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO
CC TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY
CC SIMILARITY).
CC -!- PATHWAY: Pyrimidine biosynthesis; third step.
CC -!- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 2.
CC -----
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CC -----
DR EMBL; Y18930; CAB57689.1; -.
DR EMBL; AE006690; AAK40922.1; -.
DR InterPro; IPR002195; Dihydroorotase.
DR Pfam; PF00744; Dihydroorotase; 1.
DR PROSITE; PS00482; DIHYDROOROTASE_1; FALSE_NEG.
DR PROSITE; PS00483; DIHYDROOROTASE_2; FALSE_NEG.
KW Pyrimidine biosynthesis; Hydrolase; Zinc; Complete proteome.
FT METAL 54 54 ZINC (POTENTIAL).
FT METAL 56 56 ZINC (POTENTIAL).
SQ SEQUENCE 390 AA; 44332 MW; F66C94D6988E41E7 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 390;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
|||:|
Db 109 YSRVDYFVY 117

RX MEDLINE=89128452; PubMed=2536924;
RA Lundrigan M.D., Friedrich M.J., Kadner R.J.;
RT "Nucleotide sequence of the Escherichia coli porin thermoregulatory
RL gene envY.";
RN Nucleic Acids Res. 17:800-800(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampaí G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RL corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
CC -!- FUNCTION: INFLUENCE OF TEMPERATURE-DEPENDENT EXPRESSION OF SEVERAL
CC E-COLI ENVELOPE PROTEINS, MOST NOTABLY THE PORINS OMPE AND OMPC
CC AND THE LAMBDA RECEPTOR, LAMB.
CC -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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CC -----
CC EMBL; X13548; CAA31900.1; -.
DR EMBL; AE000161; AAC73667.1; -.
DR EMBL; U82598; AAB40763.1; -.
DR EMBL; D90699; BAA35200.1; -.
DR PIR; S03425; S03425.
DR EcoGene; EG10268; envY.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF00165; HTH_Arac; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Transcription regulation; DNA-binding; Activator; Complete proteome.
FT DNA_BIND 165 184 H-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 61 61 N -> NR (IN REF. 1).
FT CONFLICT 93 93 MISSING (IN REF. 1).
FT CONFLICT 99 99 R -> P (IN REF. 1).
FT CONFLICT 150 150 S -> T (IN REF. 1).
SQ SEQUENCE 253 AA; 29019 MW; 8FB1554CC5C4238E CRC64;

Query Match 63.8%; Score 37; DB 1; Length 253;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9

Db 221 GYSSTSYFI 229
||| | |||
RESULT 14
YAI0_ECOLI
ID YAI0_ECOLI STANDARD; PRT; 257 AA.
AC Q47534;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yai0.
GN YAI0 OR B0358.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Nashimoto H., Saito N.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; D85613; BAA12835.1; -.
DR EMBL; AE000143; AAC73461.1; -.
DR EMBL; U73857; AAB18083.1; -.
DR EcoGene; EG13297; yai0.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 29040 MW; A6BC89571866AED8 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 257;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDY 7
||| | |||
Db 27 GYDFTDY 33

RESULT 15
PYRC_SULSO
ID PYRC_SULSO STANDARD; PRT; 390 AA.
AC Q9UX05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydroorotase (EC 3.5.2.3) (DHOase).
GN PYRC OR SSO0611 OR C08_039.
OS Sulfolobus solfataricus.


```

HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region V35 precursor;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus.";
RL EMBO J. 7:1047-1051(1988).
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CC -----
DR EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVHU35.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 63.8%; Score 37; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
Db 45 GYFTGYMH 54

RESULT 12
YHIW_ECOLI
ID YHIW_ECOLI STANDARD; PRT; 242 AA.
AC P37638;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transcriptional regulator yhiW.
GN YHIW OR B3515 OR Z4928 OR ECS4395.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL; U00039; AAB18491.1; -
DR EMBL; AE000428; AAC76540.1; -
DR EMBL; AE005577; AAG58656.1; -
DR EMBL; AP002565; BAB37818.1; -
DR EcoGene; EG12242; yhiW.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH_Arac; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Hypothetical protein; Transcription regulation; DNA-binding;
KW Complete proteome.
FT DNA_BIND 155 174 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 242 AA; 28028 MW; 40C11B74DA2F8DA5 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 242;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
Db 211 GYSSTSYFI 219

RESULT 13
ENVY_ECOLI
ID ENVY_ECOLI STANDARD; PRT; 253 AA.
AC P10805; P77778;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Porin thermoregulatory protein envY.
GN ENVY OR B0566.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

```

Query Match 67.2%; Score 39; DB 1; Length 235;
Best Local Similarity 75.0%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSFSTDYFI 9
||| |||
Db 134 YSFNDYFV 141

RESULT 8
HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -----
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CC -----
DR EMBL; J00488; AAA38519.1; -.
DR PIR; A02041; HVMS8A.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 7.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDY 7
||:||||
Db 45 GYTFTDY 51

RESULT 9
HV17_MOUSE STANDARD; PRT; 117 AA.
AC P01786;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 47A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80049769; PubMed=115869;

RA Robinson E.A., Appella E.;
RT "Amino acid sequence of a mouse myeloma immunogloblin heavy chain
RT (MOPC 47 A) with a 100-residue deletion.";
RL J. Biol. Chem. 254:11418-11430(1979).
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE,
CC LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA
CC MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A
CC LIGHT-HEAVY CHAIN DISULFIDE BOND.
DR PIR; A02069; AIMS47.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12975 MW; 0C74BE8BB154BDF4 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 117;
Best Local Similarity 55.6%; Pred. No. 7.1;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
|:|||||:
Db 26 GFTFTDYIM 34

RESULT 10
HV01_MOUSE STANDARD; PRT; 121 AA.
ID HV01_MOUSE
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 65.5%; Score 38; DB 1; Length 121;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
|:|||||:
Db 26 GYTFTNYWI 34

RESULT 11

RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
CC -1- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL; AE000247; AAC74572.1; -.
DR EMBL; D90792; BAA15173.1; ALT_INIT.
DR EcoGene; EG13797; ydeO.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH_Arac; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Hypothetical protein; Transcription regulation; DNA-binding;
KW Complete proteome.
FT DNA_BIND 153 172 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 253 AA; 28725 MW; 6898BBAA54DAA997 CRC64;

Query Match 70.7%; Score 41; DB 1; Length 253;
Best Local Similarity 70.0%; Pred. No. 4.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db II: I IIII
208 GYASTSYFIY 217

RESULT 6
HV15_MOUSE STANDARD; PRT; 136 AA.
ID HV15_MOUSE AC
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -----
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CC -----
CC EMBL; J00494; AAA38130.1; -.
DR PIR; A02042; HVMSB1.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 67.2%; Score 39; DB 1; Length 136;
Best Local Similarity 60.0%; Pred. No. 5.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db II: IIII ::
45 GYFTDYAMH 54

RESULT 7
RNS2_ANTHI STANDARD; PRT; 235 AA.
ID RNS2_ANTHI AC
AC Q38716;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease S-2 precursor (EC 3.1.27.1) (Stylar glycoprotein 2)
DE (S2-RNase).
GN S2.
OS Antirrhinum hispanicum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
OX NCBI_TaxID=49039;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Style;
RX MEDLINE=96240018; PubMed=8672882;
RA Xue Y., Carpenter R., Dickinson H.G., Coen E.S.;
RT "Origin of allelic diversity in antirrhinum S locus RNases.";
RL Plant Cell 8:805-814(1996).
CC -1- FUNCTION: SELF-INCOMPATIBILITY (SI) IS THE INHERITED ABILITY OF
CC A FLOWERING PLANT TO PREVENT SELF-FERTILIZATION BY DISCRIMINATING
CC BETWEEN SELF AND NON-SELF POLLEN DURING POLLINATION. IN MANY
CC SPECIES, SELF-INCOMPATIBILITY IS CONTROLLED BY
CC THE SINGLE, MULTIALLELIC LOCUS S.
CC -1- CATALYTIC ACTIVITY: Two-stage endonucleolytic cleavage to
CC nucleoside 3'-phosphates and 3'-phosphooligonucleotides with
CC 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: BELONGS TO THE RNASE T2 FAMILY.
CC -----
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CC -----
CC EMBL; X96465; CAA65319.1; -.
DR HSSP; P08056; 1BOL.
DR InterPro; IPR001568; RNase_T2.
DR Pfam; PF00445; ribonuclease_T2; 1.
DR PROSITE; PS00530; RNase_T2_1; 1.
DR PROSITE; PS00531; RNase_T2_2; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 235 RIBONUCLEASE S-2.
FT DISULFID 80 129 BY SIMILARITY.
FT ACT_SITE 66 66 BY SIMILARITY.
FT ACT_SITE 122 122 BY SIMILARITY.
FT ACT_SITE 126 126 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 235 AA; 26767 MW; DE86AEFAEE97D7D0 CRC64;

```
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
  rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
  BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
  WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
  ||:||||:
Db 26 GYTFTDYVM 34

RESULT 3
HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
  lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
  ||:||||:
Db 26 GYTFTDYVM 34
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RESULT 4
HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
  the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0501; HVMS96.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 70.7%; Score 41; DB 1; Length 98;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
  ||:||||:
Db 26 GYTFTDYMY 35

RESULT 5
YDEO_ECOLI STANDARD; PRT; 253 AA.
AC P76135; P76877;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transcriptional regulator ydeO.
GN YDEO OR B1499.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
  Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
  Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
  Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
  Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
  Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
  Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
  Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 6.2069 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	117	1 HV12_MOUSE	P01756 mus musculu
2	42	72.4	117	1 HV13_MOUSE	P01757 mus musculu
3	42	72.4	118	1 HV51_MOUSE	P06330 mus musculu
4	41	70.7	98	1 HV57_MOUSE	P18528 mus musculu
5	41	70.7	253	1 YDEO_ECOLI	P76135 escherichia
6	39	67.2	136	1 HV15_MOUSE	P01759 mus musculu
7	39	67.2	235	1 RNS2_ANTHI	Q38716 antirrhinum
8	38	65.5	117	1 HV14_MOUSE	P01758 mus musculu
9	38	65.5	117	1 HV17_MOUSE	P01786 mus musculu
10	38	65.5	121	1 HV01_MOUSE	P01745 mus musculu
11	37	63.8	117	1 HV1G_HUMAN	P23083 homo sapien
12	37	63.8	242	1 YHIW_ECOLI	P37638 escherichia
13	37	63.8	253	1 ENVY_ECOLI	P10805 escherichia
14	37	63.8	257	1 YAIO_ECOLI	Q47534 escherichia
15	37	63.8	390	1 PYRC_SULSO	Q9ux05 sulfolobus
16	37	63.8	497	1 G6PI_LEGPN	Q9rdy2 legionella
17	37	63.8	519	1 CP5V_CANAP	P43083 candida api
18	37	63.8	519	1 CP5W_CANAP	Q12573 candida api
19	36	62.1	104	1 Y376_MYCGE	P47616 mycoplasma
20	36	62.1	117	1 HV04_MOUSE	P01748 mus musculu
21	36	62.1	117	1 HV06_MOUSE	P01750 mus musculu
22	36	62.1	117	1 HV09_MOUSE	P01753 mus musculu
23	36	62.1	117	1 HV10_MOUSE	P01754 mus musculu
24	36	62.1	117	1 HV49_MOUSE	P06328 mus musculu
25	36	62.1	120	1 HV1H_HUMAN	P80421 homo sapien
26	36	62.1	120	1 HV50_MOUSE	P06329 mus musculu
27	36	62.1	139	1 HV07_MOUSE	P01751 mus musculu
28	36	62.1	808	1 PHK1_ANASP	Q8yww1 anabaena sp
29	36	62.1	821	1 PHK_SYNY3	P74690 synechocyst
30	35	60.3	137	1 HV11_MOUSE	P01755 mus musculu
31	35	60.3	138	1 HV48_MOUSE	P03980 mus musculu
32	35	60.3	162	1 PSAF_YERPE	Q56978 yersinia pe
33	35	60.3	167	1 PSAF_YERPS	Q56981 yersinia ps

34	35	60.3	199	1 NQRE_YERPE	Q9zc45 yersinia pe
35	35	60.3	430	1 G43B_DROME	Q9v4q0 drosophila
36	35	60.3	586	1 HOL1_YEAST	P53389 saccharomyc
37	35	60.3	661	1 PDAT_YEAST	P40345 saccharomyc
38	35	60.3	705	1 C1R_HUMAN	P00736 homo sapien
39	35	60.3	726	1 PBPA_AQUAE	O66874 aquifex ao
40	34	58.6	114	1 HV00_MOUSE	P01741 mus musculu
41	34	58.6	117	1 HV05_MOUSE	P01749 mus musculu
42	34	58.6	136	1 HV01_XENLA	P20956 xenopus lae
43	34	58.6	238	1 Y834_METJA	Q58244 methanococc
44	34	58.6	249	1 APPY_ECOLI	P05052 escherichia
45	34	58.6	253	1 ADIY_ECOLI	P33234 escherichia

ALIGNMENTS

RESULT 1
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
Db 26 GYTFTDYIM 34
||:||||:

RESULT 2
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;


```
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION S43.
FT CHAIN 20 137 FRAMEWORK-1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 FRAMEWORK-2.
FT DOMAIN 55 68 FRAMEWORK-3.
FT DOMAIN 69 85 JH2 SEGMENT.
FT DOMAIN 86 117 BY SIMILARITY.
FT DOMAIN 118 122
FT DOMAIN 123 137
FT DISULFID 41 115
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 53.6%; Score 52; DB 1; Length 137;
Best Local Similarity 60.0%; Pred. No. 0.15;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
   ||| :| | :| | :| |
Db 70 IDPNSGGTTYNEHFR 84

RESULT 14
HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
DR EMBL; J00536; AAA38605.1; -.
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;
```

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Query Match 52.6%; Score 51; DB 1; Length 117;
Best Local Similarity 52.9%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 4; Indels 4; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
   :| | :| | | | | :|
Db 69 NIYPSDSETHYNQKFKD 85

RESULT 15
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982);
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR; A02028; HVMSG7.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 52.6%; Score 51; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 0.19;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
   | :| | | | | :| :|
Db 50 INPGNGYTKYNEKFK 64
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Search-completed: March 10, 2003, 16:57:49
Job time : 11.5517 secs


```
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RL lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 56.7%; Score 55; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 0.043;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 51 INPSNGGTNYNEKFK 65

RESULT 9
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
CC EMBL; J00533; AAA38602.1; -.
DR PIR; C02034; HVMS45.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 55.7%; Score 54; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.06;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

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Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 70 IDPNSGGTKYNEKFK 84

RESULT 10
HV10_MOUSE
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 145 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
CC EMBL; J00533; AAA38602.1; -.
DR PIR; C02034; HVMS45.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 55.7%; Score 54; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.06;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 70 IDPNSGGTKYNEKFK 84

RESULT 11
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```



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RN
RP
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL rearrangements in heavy chain V-region gene segments.";
CC Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; LMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 69.1%; Score 67; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00047;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
||:| || |||||
Db 50 DINPNNGGTSYNQKFK 65

RESULT 3
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=84182519; PubMed=6201362;
Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
"Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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EMBL; J00494; AAA38130.1; -.
PIR; A02042; HVMSB1.
HSSP; P01772; 2PB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 64.9%; Score 63; DB 1; Length 136;
Best Local Similarity 73.3%; Pred. No. 0.0025;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
| ||:|||||
Db 70 ISTYNGTTSYNQKFK 84

RESULT 5
HV14_MOUSE
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
"Diversity of germ-line immunoglobulin VH genes.";
Nature 292:426-430(1981).
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RESULT 4
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=82222262; PubMed=6806821;
Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
"Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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EMBL; J00494; AAA38130.1; -.
PIR; A02042; HVMSB1.
HSSP; P01772; 2PB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 64.9%; Score 63; DB 1; Length 136;
Best Local Similarity 73.3%; Pred. No. 0.0025;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
| ||:|||||
Db 70 ISTYNGTTSYNQKFK 84

RESULT 5
HV14_MOUSE
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
"Diversity of germ-line immunoglobulin VH genes.";
Nature 292:426-430(1981).
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 10.5517 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	69.1	117	1 HV12_MOUSE	P01756 mus musculu
2	67	69.1	117	1 HV13_MOUSE	P01757 mus musculu
3	67	69.1	118	1 HV51_MOUSE	P06330 mus musculu
4	63	64.9	136	1 HV15_MOUSE	P01759 mus musculu
5	62	63.9	117	1 HV14_MOUSE	P01758 mus musculu
6	55	56.7	117	1 HV04_MOUSE	P01748 mus musculu
7	55	56.7	117	1 HV49_MOUSE	P06328 mus musculu
8	55	56.7	120	1 HV50_MOUSE	P06329 mus musculu
9	54	55.7	117	1 HV09_MOUSE	P01753 mus musculu
10	54	55.7	117	1 HV10_MOUSE	P01754 mus musculu
11	54	55.7	139	1 HV07_MOUSE	P01751 mus musculu
12	52	53.6	117	1 HV06_MOUSE	P01750 mus musculu
13	52	53.6	137	1 HV11_MOUSE	P01755 mus musculu
14	51	52.6	117	1 HV05_MOUSE	P01749 mus musculu
15	51	52.6	120	1 HV03_MOUSE	P01747 mus musculu
16	48	49.5	138	1 HV48_MOUSE	P03980 mus musculu
17	47	48.5	117	1 HV1B_HUMAN	P01743 homo sapien
18	46	47.4	140	1 HV02_MOUSE	P01746 mus musculu
19	46	47.4	611	1 IF4B_HUMAN	P23588 homo sapien
20	46	47.4	1302	1 RPOB_SPICI	P47767 spiroplasma
21	45	46.4	117	1 HV52_MOUSE	P06327 mus musculu
22	44	45.4	117	1 HV1G_HUMAN	P23083 homo sapien
23	44	45.4	563	1 SYR_STRPN	Q54869 streptococc
24	43	44.3	247	1 DLX6_BRARE	Q98877 brachydanio
25	43	44.3	720	1 CATA_HALN1	O73955 halobacteri
26	43	44.3	960	1 CSEL_YEAST	P33307 saccharomyc
27	42	43.3	503	1 HCK_RAT	P50545 rattus norv
28	42	43.3	524	1 HCK_MOUSE	P08103 mus musculu
29	41.5	42.8	183	1 UBCH_HUMAN	P37286 homo sapien
30	41	42.3	508	1 GALT_BACHD	Q9kdv2 bacillus ha
31	41	42.3	4349	1 FAT2_HUMAN	Q9nyq8 homo sapien
32	41	42.3	4351	1 FAT2_RAT	O88277 rattus norv
33	40	41.2	189	1 PMVK_DROME	Q9vit2 drosophila

34	40	41.2	211	1	HET3_RADMG	Q9u6x1 radianthus
35	40	41.2	317	1	YM91_YEAST	Q04867 saccharomyc
36	40	41.2	334	1	CHM1_MOUSE	Q9zlf6 mus musculu
37	40	41.2	335	1	CHM1_BOVIN	P17404 bos taurus
38	40	41.2	624	1	YH19_YEAST	P38900 saccharomyc
39	40	41.2	697	1	YHF0_YEAST	P38721 saccharomyc
40	40	41.2	805	1	SUS1_TULGE	Q41608 tulipa gesn
41	40	41.2	1080	1	HDA4_CHICK	P83038 gallus gall
42	40	41.2	1374	1	YMN3_YEAST	Q03099 saccharomyc
43	40	41.2	1859	1	YRF6_YEAST	P53819 saccharomyc
44	40	41.2	1876	1	GLS1_YEAST	P38631 saccharomyc
45	39.5	40.7	714	1	NCPR_CATRO	Q05001 catharanthu

ALIGNMENTS

RESULT 1

HV12_MOUSE

ID	HV12_MOUSE	STANDARD;	PRT;	117 AA.
AC	P01756;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ig heavy chain V region MOPC 104E.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			

SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.

MEDLINE=83075344; PubMed=6816276;

Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,

Hood L.E.;

"Complete amino acid sequence of a mouse mu chain: homology among

heavy chain constant region domains.";

Biochemistry 21:5415-5424(1982).

-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA

PROTEIN HAS ALSO BEEN DETERMINED.

-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

PIR; A02039; MHMS4E.

HSSP; P01789; IMCP.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Glycoprotein.

DISULFID 22 96 BY SIMILARITY.

CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).

NON_TER 117 117

SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match

Best Local Similarity 69.1%; Score 67; DB 1; Length 117;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16

Db 50 DINPNNGGTSYNQKFK 65

RESULT 2

HV13_MOUSE

ID	HV13_MOUSE	STANDARD;	PRT;	117 AA.
AC	P01757;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region J558.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			

RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026136; PubMed=9806840;
RA West A., Vojta P.J., Welch D.R., Weissman B.E.;
RT "Chromosome localization and genomic structure of the KiSS-1
RL metastasis suppressor gene (KiSS1).";
RL Genomics 54:145-148(1998).
RN [4]
RP ACTION ON BREAST CARCINOMA.
RX MEDLINE=97336019; PubMed=9192814;
RA Lee J.-H., Welch D.R.;
RT "Suppression of metastasis in human breast carcinoma MDA-MB-435 cells
RT after transfection with the metastasis suppressor gene, KiSS-1.";
RL Cancer Res. 57:2384-2387(1997).
CC -!- FUNCTION: METASTASIS SUPPRESSOR IN MALIGNANT MELANOMA AND IN
CC SOME HUMAN BREAST CANCERS. MAY REGULATE EVENTS DOWNSTREAM OF
CC CELL-MATRIX ADHESION, PERHAPS INVOLVING CYTOSKELETAL
CC REORGANIZATION.
CC -----
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CC -----
DR EMBL; U43527; AAC79512.1; -.
DR Genew; HGNC:6341; KiSS1.
DR MIM; 603286; -.
SQ SEQUENCE 145 AA; 15391 MW; 7B482C7436FF3BFF CRC64;

Query Match 100.0%; Score 21; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. NO. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 118 GLRF 121

Search completed: March 10, 2003, 16:57:50
Job time : 3.48276 secs

```
DE Hypothetical protein yran.
GN YRAN OR B3148.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MGI655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SIMILARITY: BELONGS TO THE UPF0102 FAMILY. STRONG, TO H.INFLUENZAE
CC HI1656.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U18997; AAA57951.1; -.
DR EMBL; AE000396; AAC76182.1; -.
DR EcoGene; EG12779; yran.
DR InterPro; IPR003509; UPF0102.
DR Pfam; PF02021; UPF0102; 1.
DR TIGRFAMs; TIGR00252; TIGR00252; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 131 AA; 14798 MW; 6A1FE67748374475 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 35 GLRF 38

RESULT 14
CRCB_XYLFA STANDARD; PRT; 143 AA.
AC Q9PDC5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein crcb homolog.
GN CRCB OR XF1454.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
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RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE CRCB FAMILY.
CC -----
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CC -----
DR EMBL; AE003975; AAF84263.1; ALT_INIT.
DR InterPro; IPR003691; Camphor_CRCB.
DR Pfam; PF02537; CRCB; 1.
KW Transmembrane; Complete proteome.
FT TRANSMEM 4 26 POTENTIAL.
FT TRANSMEM 38 60 POTENTIAL.
FT TRANSMEM 75 97 POTENTIAL.
FT TRANSMEM 104 126 POTENTIAL.
SQ SEQUENCE 143 AA; 15691 MW; 325677C2FEC41580 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 22 GLRF 25

RESULT 15
KISL_HUMAN STANDARD; PRT; 145 AA.
ID KISL_HUMAN
AC Q15726;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Malignant melanoma metastasis-suppressor KISS-1.
GN KISS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97099426; PubMed=8944003;
RA Lee J.-H., Miele M.E., Hicks D.J., Phillips K.K., Trent J.M.,
RA Weissman B.E., Welch D.R.;
RT "KISS-1, a novel human malignant melanoma metastasis-suppressor
RT gene.";
RL J. Natl. Cancer Inst. 88:1731-1737(1996).
RN [2]
RP ERRATUM.
RA Lee J.-H., Miele M.E., Hicks D.J., Phillips K.K., Trent J.M.,
RA Weissman B.E., Welch D.R.;
RA J. Natl. Cancer Inst. 89:1549-1549(1997).
```

DR StyGene; SG????; secE.
DR InterPro; IPR001901; SecE.
DR InterPro; IPR004819; SecE_bac.
DR Pfam; PF00584; SecE; 1.
DR ProDom; PD005139; SecE_bac; 1.
DR TIGRFAMs; TIGR00964; 3a0501s06; 1.
DR PROSITE; PS01067; SECE_SEC61G; 1.
KW Protein transport; Translocation; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 18 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 19 36 PROBABLE.
FT DOMAIN 37 44 PERIPLASMIC (PROBABLE).
FT TRANSMEM 45 63 PROBABLE.
FT DOMAIN 64 92 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 93 111 PROBABLE.
FT DOMAIN 112 127 PERIPLASMIC (PROBABLE).
SQ SEQUENCE 127 AA; 13689 MW; 640DB5C2080E775D CRC64;

Query Match 100.0%; Score 21; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 124 GLRF 127

RESULT 11
UCR7_KLULA
ID UCR7_KLULA STANDARD; PRT; 127 AA.
AC P49345;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ubiquinol-cytochrome c reductase complex 14 kDa protein (EC 1.10.2.2)
DE (Complex III subunit VII).
GN QCR7.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-11140;
RX MEDLINE=95035106; PubMed=7948033;
RA Mulder W., Scholten I.H., van Roon H., Grivell L.A.;
RT "Isolation and characterisation of the linked genes APA2 and QCR7,
RT coding for Ap4A phosphorylase II and the 14 kDa subunit VII of the
RT mitochondrial bcl-complex in the yeast Kluyveromyces lactis.";
RL Biochim. Biophys. Acta 1219:719-723(1994).
CC -!- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C
CC REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH
CC IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN. THIS COMPONENT
CC IS INVOLVED IN REDOX-LINKED PROTON PUMPING.
CC -!- CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
CC ferrocycytochrome c.
CC -!- SUBUNIT: FUNGI BCL COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY
CC SUBUNITS, 2 CORE PROTEINS AND 5 LOW-MOLECULAR WEIGHT PROTEINS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (Potential).
CC -!- SIMILARITY: BELONGS TO THE UQCRB/QCR7 FAMILY.

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CC EMBL; X76027; CAA53617.1; -.
DR InterPro; IPR003197; UCR_14kDa.
DR Pfam; PF02271; UCR_14kD; 1.

KW Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
KW Oxidoreductase.
SQ SEQUENCE 127 AA; 14663 MW; 7195CD85B3418876 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 42 GLRF 45

RESULT 12
H3_LEIIN
ID H3_LEIIN STANDARD; PRT; 129 AA.
AC P40285;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Histone H3.
OS Leishmania infantum.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5671;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEM 75 / Zymodeme 1;
RX MEDLINE=95002171; PubMed=7918653;
RA Soto M., Requena J.M., Morales G., Alonso C.;
RT "The Leishmania infantum histone H3 possesses an extremely divergent
RT N-terminal domain."
RL Biochim. Biophys. Acta 1219:533-535(1994).
CC -!- FUNCTION: HISTONE H3, ALONG WITH HISTONE H4, PLAYS A CENTRAL ROLE
CC IN NUCLEOSOME FORMATION.
CC -!- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATIVELY 146 BP OF DNA.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H3 FAMILY.

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CC EMBL; X77591; CAA54693.1; -.
DR PIR; S42034; S42034.
DR InterPro; IPR000164; Histone_H3.
DR InterPro; IPR004822; Histone_core.
DR Pfam; PF00125; histone; 1.
DR SMART; SM00428; H3; 1.
DR PROSITE; PS00322; HISTONE_H3_1; FALSE_NEG.
DR PROSITE; PS00959; HISTONE_H3_2; 1.
KW Nuclear protein; Chromosomal protein; DNA-binding; Nucleosome core.
SQ SEQUENCE 129 AA; 14629 MW; C8AB2EA73C906100 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 75 GLRF 78

RESULT 13
YRAN_ECOLI
ID YRAN_ECOLI STANDARD; PRT; 131 AA.
AC P45465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [6]
RP TOPOLOGY.
RX MEDLINE=91266903; PubMed=2050112;
RA Schatz P.J., Bieker K.L., Ottemann K.M., Silhavy T.J., Beckwith J.;
RT "One of three transmembrane stretches is sufficient for the
RT functioning of the SecE protein, a membrane component of the E. coli
RT secretion machinery.";
RL EMBO J. 10:1749-1757(1991).
RN [7]
RP SUBUNITS.
RX MEDLINE=20402345; PubMed=10944122;
RA Yahr T.L., Wickner W.T.;
RT "Evaluating the oligomeric state of SecYEG in preprotein
RT translocase.";
RL EMBO J. 19:4393-4401(2000).
RN [8]
RP SUBUNITS.
RX MEDLINE=20164453; PubMed=10698927;
RA Manting E.H., van Der Does C., Remigy H., Engel A., Driessen A.J.;
RT "SecYEG assembles into a tetramer to form the active protein
RT translocation channel.";
RL EMBO J. 19:852-861(2000).
RN [9]
RP MUTANTS.
RX MEDLINE=95196752; PubMed=7889938;
RA Flower A.M., Osborne R.S., Silhavy T.J.;
RT "The allele-specific synthetic lethality of prlA-prlG double mutants
RT predicts interactive domains of SecY and SecE.";
RL EMBO J. 14:884-893(1995).
CC -!- FUNCTION: ESSENTIAL FOR PROTEIN EXPORT.
CC -!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECY. THE
CC TRANSLOCATION CHANNEL SEEMS TO BE COMPOSED OF A SECA HOMODIMER AND
CC FOUR COPIES OF A SECYEG COMPLEX.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: BELONGS TO THE SECE/SEC61-GAMMA FAMILY.
CC -----
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CC -----
DR EMBL; M30610; AAA24621.1; -.
DR EMBL; U00006; AAC43079.1; -.
DR EMBL; AE000472; AAC76955.1; -.
DR EMBL; AE005629; AAG59177.1; -.
DR EMBL; AP002567; BAB38327.1; -.
DR PIR; A35139; VXPCESE.
DR PIR; S16341; S16341.
DR EcoGene; EG10939; secE.
DR InterPro; IPR001901; SecE.
DR InterPro; IPR004819; SecE_bac.
DR Pfam; PF00584; SecE; 1.
DR ProDom; PD005139; SecE_bac; 1.
DR TIGRFAMs; TIGR00964; 3a0501s06; 1.
DR PROSITE; PS01067; SECE_SEC61G; 1.
KW Protein transport; Translocation; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 18 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 19 36 PROBABLE.
FT DOMAIN 37 44 PERIPLASMIC (PROBABLE).
FT TRANSMEM 45 63 PROBABLE.
FT DOMAIN 64 92 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 93 111 PROBABLE.

FT DOMAIN 112 127 PERIPLASMIC (PROBABLE).
SQ SEQUENCE 127 AA; 13643 MW; 94D37280522875CE CRC64;

Query Match 100.0%; Score 21; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|||||
Db 124 GLRF 127

RESULT 10
SECE_SALTY STANDARD; PRT; 127 AA.
AC Q9L9K1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Preprotein translocase secE subunit.
GN SECE OR STM4147 OR STMf1.6 OR STY3738.
OS Salmonella typhimurium, and
OC Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
CC -!- FUNCTION: ESSENTIAL FOR PROTEIN EXPORT (By similarity).
CC -!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECY. THE
CC TRANSLOCATION CHANNEL SEEMS TO BE COMPOSED OF A SECA HOMODIMER AND
CC FOUR COPIES OF A SECYEG COMPLEX (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SECE/SEC61-GAMMA FAMILY.
CC -----
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CC -----
DR EMBL; AF170176; AAF33494.1; -.
DR EMBL; AE008893; AAL22975.1; -.
DR EMBL; AL627279; CAD09493.1; -.


```
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: SOME, TO E.COLI YIHN.
CC -----
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CC -----
DR EMBL; U67488; AAB98332.1; -.
DR TIGR; MJ0342; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 123 AA; 14008 MW; E2463D19323D5919 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 55 GLRF 58

RESULT 8
G8_HUMAN
ID G8_HUMAN STANDARD; PRT; 126 AA.
AC Q9UBA6; Q9UBA8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G8 protein.
GN G8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93206277; PubMed=8096093;
RA Partanen J., Milner C., Campbell R.D., Maki M., Lipsanen V.,
RA Koskimies S.;
RT "HLA-linked heat-shock protein 70 (HSP70-2) gene polymorphism and
RT celiac disease.";
RL Tissue Antigens 41:15-19(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Partanen J., Campbell R.D.;
RT "Characterization of the novel gene G8 located in the class III region
RT of the human major histocompatibility complex.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; G8 (SHOWN HERE) AND G8.1; MAY BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -----
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```

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CC -----
DR EMBL; AJ249732; CAB56508.1; -.
DR EMBL; AJ249731; CAB56506.1; -.
DR MIM; 605447; -.
KW Alternative splicing.
FT VARSPLIC 86 126
FT MNSGSPARDNAPSQRFCNLSSEGLRFGISPSWREALYGCCHA
FT -> SCKTFIAVLSLSKSKE (IN ISOFORM G8.1).
SQ SEQUENCE 126 AA; 13270 MW; 59610E786B9C4F60 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 108 GLRF 111

RESULT 9
SECE_ECOLI
ID SECE_ECOLI STANDARD; PRT; 127 AA.
AC P16920;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Preprotein translocase sece subunit.
GN SECE OR PRLG OR B3981 OR Z5554 OR ECS4904.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90170882; PubMed=2137819;
RA Downing W.L., Sullivan S.L., Gottesman M.E., Dennis P.P.;
RT "Sequence and transcriptional pattern of the essential Escherichia
RT coli sece-nusG operon.";
RL J. Bacteriol. 172:1621-1627(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378734; PubMed=2673920;
RA Schatz P.J., Riggs P.D., Jacq A., Fath M.J., Beckwith J.;
RT "The sece gene encodes an integral membrane protein required for
RT protein export in Escherichia coli.";
RL Genes Dev. 3:1035-1044(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes.";
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
```

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 89 GLRF 92

RESULT 5
IM09_MESCR
ID IM09_MESCR STANDARD; PRT; 93 AA.
AC Q9XGX8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit Tim9.
GN TIM9.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RA Bauer M.F., Brunner M., Hofmann S.;
RT "Cloning and mapping of the Tim10/DDP gene family encoding small zinc
RT finger proteins involved in mitochondrial carrier import.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -----
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CC -----
CC EMBL; AF150112; AAD40018.1; -
CC InterPro; IPR004217; 2nf_Tim10/DDP.
DR Pfam; PF02953; zf-Tim10_DDP; 1.
DR Transport; Protein transport; Translocation; Mitochondrion;
KW Inner membrane.
KW SEQUENCE 93 AA; 10878 MW; D5FB1952CEAF48E9 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 79 GLRF 82

RESULT 6
CFP6_MYCTU
ID CFP6_MYCTU STANDARD; PRT; 112 AA.
AC O53251;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Low molecular weight protein antigen 6 (CFP-6).
GN CFP6 OR RV3004 OR MT3084.1 OR MTV012.18.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriia (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
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RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 5-16.
RC STRAIN=H37RV;
RA Bhaskar S., Mukherjee R.;
RT "Isolation, purification and immunological characterization of low
RT molecular weight protein antigens from culture filtrate of
RT M. tuberculosis.";
RL Submitted (NOV-1998) to the SWISS-PROT data bank.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- CAUTION: THE INITIATOR METHIONINE MAY BE FURTHER UPSTREAM MAKING
CC THE SEQUENCE A PRECURSOR.
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CC -----
CC EMBL; AL021287; CAA16089.1; -
CC EMBL; AE007128; -; NOT_ANNOTATED_CDS.
DR TIGR; MT3084.1; -.
DR TubercuList; Rv3004; -.
KW Antigen; Complete proteome.
FT CONFLICT 9 L -> F (IN REF. 3).
SQ SEQUENCE 112 AA; 12223 MW; 0094564796B29AEB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 67 GLRF 70

RESULT 7
Y342_METJA
ID Y342_METJA STANDARD; PRT; 123 AA.
AC Q57788;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0342.
GN MJ0342.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
```

DE Mitochondrial import inner membrane translocase subunit Tim9.
GN TIM9.
OS Zygosaccharomyces baillii.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
OX NCBI_TaxID=4954;
RN [1]
RP SEQUENCE FROM N.A.
RA Mollapour M., Piper P.W.;
RT "Targeted gene deletion in Zygosaccharomyces baillii.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
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CC -----
CC EMBL; AF279260; AAG17695.1;
DR InterPro; IPR004217; Znf_Tim10/DDP.
DR Pfam; PF02953; zf-Tim10-DDP; 1.
KW Transport; Protein transport; Translocation; Mitochondrion;
KW Inner membrane.
SQ SEQUENCE 87 AA; 10198 MW; BBAB2C5D909347CD CRC64;

Query Match 100.0%; Score 21; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 71 GLRF 74

RESULT 3
YPB2_ECOLI STANDARD; PRT; 87 AA.
AC P03850;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hypothetical 10.0 kDa protein.
OS Escherichia coli.
OG Plasmid pBR322.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80002802; Pubmed=383387;
RA Sutcliffe J.G.;
RT "Complete nucleotide sequence of the Escherichia coli plasmid
RT pBR322.";
RL Cold Spring Harb. Symp. Quant. Biol. 43:77-90(1979).
CC -----
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CC -----
CC EMBL; J01749; -; NOT_ANNOTATED_CDS.
DR PIR; A04479; Q0EC2.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 87 AA; 10035 MW; D665A3EAC7129D4F CRC64;

Query Match 100.0%; Score 21; DB 1; Length 87;

Best Local Similarity 100.0%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 18 GLRF 21

RESULT 4
DPM3_MOUSE STANDARD; PRT; 92 AA.
ID DPM3_MOUSE
AC Q9D1Q4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dolichol-phosphate mannosyltransferase subunit 3 (Dolichol-phosphate
DE mannose synthase subunit 3) (Dolichyl-phosphate beta-D-
DE mannosyltransferase subunit 3) (Mannose-P-dolichol synthase subunit 3)
DE (MPD synthase subunit 3) (DPM synthase complex subunit 3).
GN DPM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Stabilizer subunit of the dolichol-phosphate-mannose
CC synthase complex (By similarity).
CC -!- SUBUNIT: Composed of three subunits; DPM1, DPM2 and DPM3.
CC Associated with DPM1 via its C-terminal domain and with DPM2 via
CC its N-terminal portion (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DPM3 FAMILY.
CC -----
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CC -----
CC EMBL; AK003223; BAB22652.1;
DR MGD; MGI:1915813; 1110001H19Rik.
KW Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 37 57 POTENTIAL.
SQ SEQUENCE 92 AA; 10139 MW; B621E6E47337CC40 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 92;

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 2.48276 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	76	1 Y4MF_RHISN	P55565 rhizobium s
2	21	100.0	87	1 IM09_ZYGBA	P57745 zygosacchar
3	21	100.0	87	1 YPB2_ECOLI	P03850 escherichia
4	21	100.0	92	1 DPM3_MOUSE	Q9dlq4 m dolichol-
5	21	100.0	93	1 IM09_MESCR	Q9xgx8 mesembryant
6	21	100.0	112	1 CFP6_MYCTU	O53251 mycobacteri
7	21	100.0	123	1 Y342_METJA	Q57788 methanococc
8	21	100.0	126	1 G8_HUMAN	Q9uba6 homo sapien
9	21	100.0	127	1 SECE_ECOLI	P16920 escherichia
10	21	100.0	127	1 SECE_SALTY	Q9l9k1 salmonella
11	21	100.0	127	1 UCR7_KLULA	P49345 kluuveromyc
12	21	100.0	129	1 H3_LEITN	P40285 leishmania
13	21	100.0	131	1 YRAN_ECOLI	P45465 escherichia
14	21	100.0	143	1 CRCB_XYLFA	Q9pdc5 xylella fas
15	21	100.0	145	1 KIS1_HUMAN	Q15726 homo sapien
16	21	100.0	147	1 MSRB_VIBCH	Q9kqk0 vibrio chol
17	21	100.0	151	1 HUTP_PACSU	P10943 bacillus su
18	21	100.0	154	1 RISB_AQUAE	O66529 aquifex aeo
19	21	100.0	161	1 Y709_PYRHO	O58440 pyrococcus
20	21	100.0	162	1 HBL_HORVU	Q42831 hordeum vul
21	21	100.0	163	1 YC72_METJA	Q58668 methanococc
22	21	100.0	165	1 HBL_MAIZE	Q9fy42 zea mays (m
23	21	100.0	165	1 HBL_ZEAMP	Q9m593 zea mays (s
24	21	100.0	169	1 HBL2_ORYSA	O04985 oryza sativ
25	21	100.0	175	1 FANH_ECOLI	P20862 escherichia
26	21	100.0	176	1 PACA_HUMAN	P18509 h pituitary
27	21	100.0	176	1 PACA_SHEEP	P16613 o pituitary
28	21	100.0	178	1 YE57_HAFIN	Q57201 haemophilus
29	21	100.0	179	1 YORI_ADEG1	P20743 avian adeno
30	21	100.0	180	1 ARF1_CHLRE	P51821 chlamydomon
31	21	100.0	180	1 RL5_CHLMU	Q9pjm6 chlamydia m
32	21	100.0	180	1 RL5_CHLPN	Q9z7r9 chlamydia p
33	21	100.0	180	1 RL5_CHLTR	P28531 chlamydia t

34	21	100.0	186	1 ARL_SCHPO	Q09767 schizosacch
35	21	100.0	197	1 YF79_ARCFU	O28693 archaeoglob
36	21	100.0	198	1 GSPJ_KLEPN	P15749 klebsiella
37	21	100.0	198	1 VCO7_ADE02	P03266 human adeno
38	21	100.0	199	1 CAST_SOLTU	Q09011 solanum tub
39	21	100.0	208	1 GLTP_BOVIN	P17403 bos taurus
40	21	100.0	208	1 GLTP_HUMAN	Q9nzd2 homo sapien
41	21	100.0	208	1 GLTP_MOUSE	Q9jl62 mus musculu
42	21	100.0	209	1 VAD2_TREPA	O83539 treponema p
43	21	100.0	212	1 NOG2_BRARE	Q9w740 brachydanio
44	21	100.0	218	1 GPH_RHOSH	P95650 rhodobacter
45	21	100.0	219	1 RR3_ASTLO	P58133 astasia lon

ALIGNMENTS

RESULT 1					
Y4MF_RHISN					
ID Y4MF_RHISN	STANDARD;	PRT;	76 AA.		
AC P55565;					
DT 01-NOV-1997 (Rel. 35, Created)					
DT 01-NOV-1997 (Rel. 35, Last sequence update)					
DT 01-NOV-1997 (Rel. 35, Last annotation update)					
DE Hypothetical transcriptional regulator Y4MF.					
GN Y4MF.					
OS Rhizobium sp. (strain NGR234).					
OG Plasmid sym pNGR234a.					
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;					
OC Rhizobiaceae; Rhizobium.					
OX NCBI_TaxID=394;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=97305956; PubMed=9163424;					
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,					
RA Perret X.;					
RT "Molecular basis of symbiosis between Rhizobium and legumes.";					
RL Nature 387:394-401(1997).					
CC -!- SIMILARITY: LOW, TO PHAGE P22 REPRESSOR PROTEIN C2 AND PHAGE P2					
CC REPRESSOR PROTEIN C.					

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DR EMBL; AE000085; AAB91769.1; -.					
DR InterPro; IPR001387; HTH_3.					
DR Pfam; PF01381; HTH_3; 1.					
DR SMART; SM00530; HTH_XRE; 1.					
KW Hypothetical protein; Transcription regulation; DNA-binding; Plasmid.					
FT DNA BIND 25 44					
SQ SEQUENCE 76 AA; 8205 MW; A2FE50FC6E518D23 CRC64;					

Query Match 100.0%; Score 21; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLRF 4
Db	36	GLRF 39

RESULT 2					
IM09_ZYGBA					
ID IM09_ZYGBA	STANDARD;	PRT;	87 AA.		
AC P57745;					
DT 16-OCT-2001 (Rel. 40, Created)					
DT 16-OCT-2001 (Rel. 40, Last sequence update)					
DT 16-OCT-2001 (Rel. 40, Last annotation update)					

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RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RL";
RL Science 286:1571-1577(1999).
DR EMBL; AE002007; AAF11201.1; -.
DR TIGR; DR1640; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 63 AA; 6982 MW; 116456AA28DDDD5BD CRC64;

Query Match 100.0%; Score 21; DB 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 8 GLRF 11

RESULT 14

Q8S140
ID Q8S140 PRELIMINARY; PRT; 70 AA.
AC Q8S140;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P0415A04.1 protein.
GN P0415A04.1.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
RT clone:P0415A04.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP003345; BAB90093.1; -.
SQ SEQUENCE 70 AA; 8046 MW; 761A5B711F5663B5 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 22 GLRF 25

RESULT 15

Q9LNZ1
ID Q9LNZ1 PRELIMINARY; PRT; 71 AA.
AC Q9LNZ1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE F9C16.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kieleczawa J., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,

RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
RA Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F9C16 from chromosome
RT I.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC022314; AAF79670.1; -.
SQ SEQUENCE 71 AA; 8435 MW; 8AD3B9A8924B1E2A CRC64;

Query Match 100.0%; Score 21; DB 10; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 38 GLRF 41

Search completed: March 10, 2003, 17:00:14
Job time : 10.8276 secs

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OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SBW25;
RA Preston G.M., Bertrand N., Rainey P.B.;
RT "Type III secretion in plant growth-promoting Pseudomonas fluorescens
RT SBW25.";
RL Mol. Microbiol. 0:0-0(2001).
DR EMBL; AY038582; AAK74144.1; -.
KW Hypothetical protein.
SQ SEQUENCE 58 AA; 6584 MW; 312FA3FC60385E4D CRC64;

Query Match 100.0%; Score 21; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 7 GLRF 10

RESULT 10
Q8VX80
ID Q8VX80 PRELIMINARY; PRT; 58 AA.
AC Q8VX80;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 6.4 kDa protein (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT;
RA Dubos C., Plomion C.;
RT "Identification of water-deficit responsive genes in maritime pine
RT (Pinus pinaster Ait.) roots using non radioactive cDNA-AFLP.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ300727; CAC83311.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6392 MW; ACC4333733EE41A7 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 46 GLRF 49

RESULT 11
Q90VY6
ID Q90VY6 PRELIMINARY; PRT; 59 AA.
AC Q90VY6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Survivin gamma (Survivin short).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Langer J.S., Bridgham J.T., Johnson A.L.;
```

```
RT "Molecular cloning and characterization of novel chicken survivin
RT splicing variants.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF377324; AAK56309.1; -.
DR EMBL; AF377322; AAK56307.1; -.
SQ SEQUENCE 59 AA; 6716 MW; 79FE9B7DA6C2A2CA CRC64;

Query Match 100.0%; Score 21; DB 13; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 48 GLRF 51

RESULT 12
Q9I6K6
ID Q9I6K6 PRELIMINARY; PRT; 60 AA.
AC Q9I6K6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA0284.
GN PA0284.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004466; AAG03673.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 60 AA; 6733 MW; 5F0889358D97FA57 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 26 GLRF 29

RESULT 13
Q9RTW3
ID Q9RTW3 PRELIMINARY; PRT; 63 AA.
AC Q9RTW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein DR1640.
GN DR1640.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
```

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627277; CAD02943.1; -.
DR PROSITE; IPR001230; Prenyl_site.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 39 AA; 4450 MW; CF0A930C832A41B3 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 5 GLRF 8

RESULT 6
Q8VJM3
ID Q8VJM3 PRELIMINARY; PRT; 41 AA.
AC Q8VJM3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein MT2369.
GN MT2369.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE007078; AAK46659.1; -.
DR TIGR; MT2369; -.
KW Hypothetical protein.
SQ SEQUENCE 41 AA; 4309 MW; 9F71B43DB6955C92 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 23 GLRF 26

RESULT 7
Q9IX54
ID Q9IX54 PRELIMINARY; PRT; 42 AA.
AC Q9IX54;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Major core protein (Fragment).
OS Possum adenovirus.

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Atadenovirus.
OX NCBI_TaxID=121816;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomson D.M., Meers J.;
RT "Molecular confirmation of an adenovirus in brushtail possums
RT (Trichosurus vulpecula).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249333; AAF65557.1; -.
DR InterPro; IPR004912; Adeno_VII.
DR Pfam; PF03228; Adeno_VII; 1.
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4765 MW; 87C1D4978D1D13EC CRC64;

Query Match 100.0%; Score 21; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 25 GLRF 28

RESULT 8
Q93VA2
ID Q93VA2 PRELIMINARY; PRT; 56 AA.
AC Q93VA2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P0487H02.23 protein (P0682B08.4 protein).
GN P0487H02.23 OR P0682B08.4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0487H02.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0682B08.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002883; BAB67863.1; -.
DR EMBL; AP003578; BAB60934.1; -.
SQ SEQUENCE 56 AA; 6501 MW; DED2A3D88ACF4C60 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 42 GLRF 45

RESULT 9
Q8VPK5
ID Q8VPK5 PRELIMINARY; PRT; 58 AA.
AC Q8VPK5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 6.6 kDa protein.
OS Pseudomonas fluorescens.

DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)				
DE	Elongation factor EF-Tu (Fragment).				
GN	TUFA.				
OS	Serratia marcescens.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OC	Serratia.				
OX	NCBI_TaxID=615;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99429862; PubMed=10498727;				
RA	Allen T., Shen P., Samsel L., Liu R., Lindahl L., Zengel J.M.;				
RT	"Phylogenetic analysis of L4-mediated autogenous control of the S10				
RT	ribosomal protein operon.";				
RL	J. Bacteriol. 181:6124-6132(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Noorani S.M., Lindahl L., Zengel J.M.;				
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF058451; AAC14291.1; -.				
DR	InterPro; IPR004160; EFTU_Cterm.				
DR	Pfam; PF03143; GTP_EFTU_D3; 1.				
FT	NON_TER 1				
SQ	SEQUENCE 26 AA; 2659 MW; 979F0015618DE7EB CRC64;				
Query Match 100.0%; Score 21; DB 2; Length 26;					
Best Local Similarity 100.0%; Pred. NO. 1.1e+02;					
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 GLRF 4				
Db	4 GLRF 7				
RESULT 3					
Q8VJT7					
ID	Q8VJT7 PRELIMINARY; PRT; 35 AA.				
AC	Q8VJT7;				
DT	01-MAR-2002 (TrEMBLrel. 20, Created)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)				
DE	Hypothetical protein MT2011.				
GN	MT2011.				
OS	Mycobacterium tuberculosis.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
OX	NCBI_TaxID=1773;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CDC 1551 / OSHKOSH;				
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,				
RA	Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,				
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,				
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,				
RA	Bishai W.;				
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and				
RT	laboratory strains.";				
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AE007054; AAK46283.1; -.				
DR	TIGR; MT2011; -.				
KW	Hypothetical protein.				
SQ	SEQUENCE 35 AA; 3901 MW; F9ED2D87A4F808F CRC64;				
Query Match 100.0%; Score 21; DB 16; Length 35;					
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;					
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 GLRF 4				
Db	7 GLRF 10				
RESULT 4					
Q9PCI9					

ID	Q9PCI9	PRELIMINARY; PRT; 37 AA.			
AC	Q9PCI9;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)				
DE	Hypothetical protein Xf1790.				
GN	Xf1790.				
OS	Xylella fastidiosa.				
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;				
OC	Xylella.				
OX	NCBI_TaxID=2371;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=9A5C;				
RX	MEDLINE=20365717; PubMed=10910347;				
RA	Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,				
RA	Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,				
RA	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,				
RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,				
RA	Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,				
RA	Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,				
RA	Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,				
RA	Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,				
RA	Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,				
RA	Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,				
RA	Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,				
RA	Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,				
RA	Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,				
RA	Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,				
RA	Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,				
RA	Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,				
RA	Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,				
RA	de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,				
RA	Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,				
RA	Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,				
RA	de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,				
RA	da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,				
RA	da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,				
RA	de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,				
RA	Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,				
RA	Zago M.A., Zatz M., Meidanis J., Setubal J.C.;				
RT	"The genome sequence of the plant pathogen Xylella fastidiosa.";				
RL	Nature 406:151-159(2000).				
DR	EMBL; AE004001; AAF84598.1; -.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 37 AA; 3952 MW; D2656E66BA48EB9E CRC64;				
Query Match 100.0%; Score 21; DB 16; Length 37;					
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;					
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 GLRF 4				
Db	3 GLRF 6				
RESULT 5					
Q8Z3T7					
ID	Q8Z3T7 PRELIMINARY; PRT; 39 AA.				
AC	Q8Z3T7;				
DT	01-MAR-2002 (TrEMBLrel. 20, Created)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)				
DE	Hypothetical protein STY3277.				
GN	STY3277.				
OS	Salmonella typhi.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OC	Salmonella.				
OX	NCBI_TaxID=601;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CT18;				
RX	MEDLINE=21534947; PubMed=11677608;				

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 8.82759 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	26	2	O68929	O68929 escherichia
2	21	100.0	26	2	O68933	O68933 serratia ma
3	21	100.0	35	16	Q8VJT7	Q8vj77 mycobacteri
4	21	100.0	37	16	Q9PCI9	Q9pci9 xylella fas
5	21	100.0	39	16	Q8Z3T7	Q8z3t7 salmonella
6	21	100.0	41	16	Q8VJM3	Q8vjm3 mycobacteri
7	21	100.0	42	12	Q9IX54	Q9ix54 possum aden
8	21	100.0	56	10	Q93VA2	Q93va2 oryza sativ
9	21	100.0	58	2	Q8VPK5	Q8vpk5 pseudomonas
10	21	100.0	58	10	Q8VX80	Q8vx80 pinus pinas
11	21	100.0	59	13	Q90VY6	Q90vy6 gallus gall
12	21	100.0	60	16	Q9I6K6	Q9i6k6 pseudomonas
13	21	100.0	63	16	Q9RTW3	Q9rtw3 deinococcus
14	21	100.0	70	10	Q8SI40	Q8sl40 oryza sativ
15	21	100.0	71	10	Q9LNZ1	Q9lnz1 arabidopsis
16	21	100.0	73	2	Q8RPP0	Q8rpp0 legionella

17	21	100.0	73	16	Q988N8	Q988n8 rhizobium l
18	21	100.0	73	16	Q8X2S9	Q8x2s9 escherichia
19	21	100.0	75	17	O27I49	O27i49 methanobact
20	21	100.0	76	12	Q842I4	Q842i4 human papil
21	21	100.0	77	16	Q92MC1	Q92mc1 rhizobium m
22	21	100.0	79	5	Q8T948	Q8t948 drosophila
23	21	100.0	80	10	Q9M0H9	Q9m0h9 arabidopsis
24	21	100.0	83	1	Q8X253	Q8x253 halobacteri
25	21	100.0	83	16	Q9K0R2	Q9k0r2 neisseria m
26	21	100.0	84	16	Q8YWD4	Q8ywd4 anabaena sp
27	21	100.0	85	2	Q9LAM7	Q9lam7 salmonella
28	21	100.0	86	2	Q936F6	Q936f6 staphylococ
29	21	100.0	88	5	Q27405	Q27405 pratylenchu
30	21	100.0	88	16	Q9I7B4	Q9i7b4 pseudomonas
31	21	100.0	89	17	Q9HPK5	Q9hpk5 halobacteri
32	21	100.0	90	4	Q9UBV1	Q9ubv1 homo sapien
33	21	100.0	91	12	Q98429	Q98429 paramecium
34	21	100.0	91	16	Q97HY6	Q97hy6 clostridium
35	21	100.0	91	16	Q92FW0	Q92fw0 rickettsia
36	21	100.0	94	16	Q8YAP4	Q8yap4 listeria mo
37	21	100.0	95	16	Q8YYS3	Q8yys3 anabaena sp
38	21	100.0	97	10	Q9LRT6	Q9lrt6 arabidopsis
39	21	100.0	97	17	Q8TRU8	Q8tru8 methanosarc
40	21	100.0	98	6	Q95N84	Q95n84 ovis aries
41	21	100.0	99	2	Q93DW6	Q93dw6 mycoplasma
42	21	100.0	99	10	Q8SAW8	Q8saw8 oryza sativ
43	21	100.0	99	17	Q9HL46	Q9hl46 thermoplasm
44	21	100.0	100	16	Q98FX9	Q98fx9 rhizobium l
45	21	100.0	101	16	Q8ZHS9	Q8zhs9 yersinia pe

ALIGNMENTS

RESULT 1
O68929 ID O68929 PRELIMINARY; PRT; 26 AA.
AC O68929;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Elongation factor EF-Tu (Fragment).
GN TUFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR30;
RA Noorani S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF058450; AAC14286.1; .
DR InterPro; IPR004160; EFTU_Cterm.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 2645 MW; 92387015618DE7EB CRC64;

Query Match 100.0%; Score 21; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
| | | |
Db 4 GLRF 7

RESULT 2
O68933 ID O68933 PRELIMINARY; PRT; 26 AA.
AC O68933;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

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ID	Q924Q1	PRELIMINARY;	PRT;	142 AA.
AC	Q924Q1;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	V23-D-J-C mu protein (Fragment).			
GN	V23-D-J-C MU.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6;			
RA	Kozono Y., Kozono H., Azuma T.;			
RT	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals			
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-			
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP).";			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB069913; BAB63929.1; -.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF00047; ig; 1.			
FT	NON_TER 1 1			
FT	NON_TER 142 142			
SQ	SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;			
Query Match 57.7%; Score 56; DB 11; Length 142;				
Best Local Similarity 56.2%; Pred. No. 0.18;				
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;				
QY	1 DIDPYNGDTSYNQKFR 16			
	: :			
Db	50 NINPSNGGTNYNERFK 65			
RESULT 14				
Q9Z1C4				
ID	Q9Z1C4	PRELIMINARY;	PRT;	118 AA.
AC	Q9Z1C4;			
DT	01-MAY-1999 (TrEMBLrel. 10, Created)			
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RA	Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,			
RA	Matis L.M., Evans M.J.;			
RT	"Humanized porcine VCAM-specific monoclonal antibodies with chimeric			
RT	IgG2/G4 constant regions block human leukocyte binding to porcine			
RT	endothelial cells.";			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U78801; AAD00293.1; -.			
DR	HSSP; P01810; 2FBJ.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
FT	NON_TER 1 1			
FT	NON_TER 118 118			
SQ	SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;			
Query Match 56.7%; Score 55; DB 11; Length 118;				
Best Local Similarity 73.3%; Pred. No. 0.21;				
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;				
QY	2 IDPYNGDTSYNQKFR 16			
	:			
Db	51 IYPGDGDTSYTQKFR 65			

RESULT 15				
Q925S2				
ID	Q925S2	PRELIMINARY;	PRT;	170 AA.
AC	Q925S2;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	MRP4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RX	PubMed=11819679;			
RA	Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,			
RA	Su C.;			
RT	"Mechanism of exogenous nucleic acids and their precursors improving			
RT	the repair of intestinal epithelium after irradiation in mice.";			
RL	World J. Gastroenterol. 6:709-717(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RA	Cui D., Zeng G., Yan X., Li X., Su C.;			
RT	"Cloning of mouse genes related to repairing of intestinal epithelium			
RT	of the irradiated mice by treatment with the intestinal RNA of mice of			
RT	the same strain.";			
RL	Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).			
DR	EMBL; AF240167; AAK43732.1; -.			
DR	InterPro; IPR003598; Ig_C2.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00408; IGC2; 1.			
KW	Immunoglobulin domain.			
SQ	SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;			
Query Match 56.7%; Score 55; DB 11; Length 170;				
Best Local Similarity 60.0%; Pred. No. 0.32;				
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;				
QY	2 IDPYNGDTSYNQKFR 16			
	: : :			
Db	53 ISTYDGNNTNYNQKFK 67			

Search completed: March 10, 2003, 17:00:12
Job time : 37.5172 secs

DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)				
DE	Anti-DNA heavy chain (Fragment).				
GN	J558.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C3H/HEJ-LPR/LPR;				
RX	MEDLINE=96409289; PubMed=8814271;				
RA	Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;				
RT	"Differences in V kappa gene utilization and VH CDR3 sequence among				
RT	anti-DNA from C3H-lpr mice and lupus mice with nephritis.";				
RL	Eur. J. Immunol. 26:2225-2233(1996).				
DR	EMBL; U59154; AAB02916.1; -.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00409; IG; 1.				
DR	SMART; SM00406; IGV; 1.				
FT	NON_TER 1				
FT	NON_TER 123 123				
SQ	SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;				
Query Match 66.0%; Score 64; DB 11; Length 123;					
Best Local Similarity 64.7%; Pred. No. 0.0074;					
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;					
QY	1 DIDPYNGDTSYNQKFRD 17				
Db	50 DINPYGGTRYSQKFKD 66				
RESULT 7					
Q96GA6					
ID	Q96GA6 PRELIMINARY; PRT; 614 AA.				
AC	Q96GA6;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)				
DE	Unknown (protein for MGC:15420).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=B-CELL;				
RA	Strausberg R.;				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; BC009851; AAH09851.1; -.				
DR	InterPro; IPR000005; HTHArac.				
DR	InterPro; IPR003598; Ig_c2.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; ig; 5.				
DR	SMART; SM00408; IGC2; 2.				
DR	PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.				
KW	Immunoglobulin domain.				
SQ	SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;				
Query Match 61.9%; Score 60; DB 4; Length 614;					
Best Local Similarity 62.5%; Pred. No. 0.22;					
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;					
QY	2 IDPYNGDTSYNQKFRD 17				
	: : :				
Db	70 ITPFNGNTNYAQKQFD 85				
RESULT 8					

Q9DCD9					
ID	Q9DCD9 PRELIMINARY; PRT; 426 AA.				
AC	Q9DCD9;				
DT	01-JUN-2001 (TrEMBLrel. 17, Created)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	Adult male kidney cDNA, RIKEN full-length enriched library,				
DE	clone:0610041A01, full insert sequence.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=KIDNEY;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee.N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,				
RA	Hayashizaki Y.;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
DR	EMBL; AK002875; BAB22422.1; -.				
DR	HSSP; P01810; 2FBJ.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003597; Ig_cl.				
DR	InterPro; IPR003600; Ig_like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; ig; 4.				
DR	SMART; SM00409; IG; 3.				
DR	SMART; SM00407; IGcl; 3.				
DR	SMART; SM00410; IG_like; 1.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.				
SQ	SEQUENCE 426 AA; 45819 MW; 56E1275BA48F6FB1 CRC64;				
Query Match 59.8%; Score 58; DB 11; Length 426;					
Best Local Similarity 90.9%; Pred. No. 0.31;					
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	6 NGDTSYNQKFR 16				
Db	17 NGDTSYNQKFK 27				
RESULT 9					
Q91WT3					
ID	Q91WT3 PRELIMINARY; PRT; 481 AA.				
AC	Q91WT3;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)				
DE	Hypothetical 52.0 kDa protein.				
GN	AI893585.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC018455; AAH18455.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 73.2%; Score 71; DB 11; Length 481;
Best Local Similarity 80.0%; Pred. No. 0.0026;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
   ||||| :|||||
Db 70 IDPYNGSSYNQKFK 84

RESULT 3
Q920E8 PRELIMINARY; PRT; 120 AA.
AC Q920E8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
   in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF307936; AAL09420.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR NON_TER 1
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 70.1%; Score 68; DB 11; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.0016;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
   :|||| :|||||
Db 50 NIDPYGGTSYNQKFK 65

RESULT 4
Q9QXF0 PRELIMINARY; PRT; 117 AA.
ID Q9QXF0
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AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 69.1%; Score 67; DB 11; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
   ||:| || |||||:
Db 50 DPNPNGGTSYNQKFK 65

RESULT 5
Q9QXE9 PRELIMINARY; PRT; 117 AA.
AC Q9QXE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 69.1%; Score 67; DB 11; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
   ||:| || |||||:
Db 50 DPNPNGGTSYNQKFK 65

RESULT 6
Q8VIJ1 PRELIMINARY; PRT; 123 AA.
ID Q8VIJ1
AC Q8VIJ1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 37.5172 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	76	78.4	488	11	Q91WR1	Q91wr1 mus musculu
2	71	73.2	481	11	Q8VCV5	Q8vcv5 mus musculu
3	68	70.1	120	11	Q920E8	Q920e8 mus musculu
4	67	69.1	117	11	Q9QXF0	Q9qxf0 mus musculu
5	67	69.1	117	11	Q9QXE9	Q9qxe9 mus musculu
6	64	66.0	123	11	Q8VIJ1	Q8vij1 mus musculu
7	60	61.9	614	4	Q96GA6	Q96ga6 homo sapien
8	58	59.8	426	11	Q9DCD9	Q9dcd9 mus musculu
9	58	59.8	481	11	Q91WT3	Q91wt3 mus musculu
10	56	57.7	109	11	Q9JL75	Q9j175 mus musculu
11	56	57.7	119	5	Q9GYZ2	Q9gyz2 schistosoma
12	56	57.7	140	11	Q924P8	Q924p8 mus musculu
13	56	57.7	142	11	Q924Q1	Q924q1 mus musculu
14	55	56.7	118	11	Q9Z1C4	Q9z1c4 mus musculu
15	55	56.7	170	11	Q925S2	Q925s2 mus musculu
16	54	55.7	137	11	Q924R6	Q924r6 mus musculu

17	54	55.7	139	11	Q924R5	Q924r5 mus musculu
18	54	55.7	140	11	Q924R2	Q924r2 mus musculu
19	54	55.7	141	11	Q924Q4	Q924q4 mus musculu
20	54	55.7	143	11	Q924R7	Q924r7 mus musculu
21	54	55.7	143	11	Q924R0	Q924r0 mus musculu
22	54	55.7	143	11	Q924Q5	Q924q5 mus musculu
23	54	55.7	143	11	Q91VA2	Q91va2 mus musculu
24	54	55.7	144	11	Q924P5	Q924p5 mus musculu
25	54	55.7	145	11	Q924R4	Q924r4 mus musculu
26	54	55.7	145	11	Q924R3	Q924r3 mus musculu
27	54	55.7	145	11	Q924R1	Q924r1 mus musculu
28	54	55.7	145	11	Q924Q9	Q924q9 mus musculu
29	54	55.7	145	11	Q924Q7	Q924q7 mus musculu
30	54	55.7	145	11	Q924Q6	Q924q6 mus musculu
31	54	55.7	145	11	Q924P7	Q924p7 mus musculu
32	54	55.7	146	11	Q924R8	Q924r8 mus musculu
33	54	55.7	146	11	Q924Q8	Q924q8 mus musculu
34	54	55.7	146	11	Q924Q3	Q924q3 mus musculu
35	52	53.6	143	11	Q924Q0	Q924q0 mus musculu
36	52	53.6	143	11	Q924P9	Q924p9 mus musculu
37	52	53.6	278	11	Q921K1	Q921k1 mus musculu
38	51	52.6	114	11	Q9JL81	Q9jl81 mus musculu
39	51	52.6	468	11	Q99L31	Q99l31 mus musculu
40	50	51.5	110	11	Q9JL77	Q9jl77 mus musculu
41	50	51.5	119	9	Q8SDV7	Q8sdv7 bacterioph
42	50	51.5	123	16	Q931Z9	Q931z9 staphylococ
43	50	51.5	143	11	Q91V67	Q91v67 mus musculu
44	48	49.5	111	11	Q9D9B8	Q9d9b8 mus musculu
45	47	48.5	124	4	Q9UL92	Q9ul92 homo sapien

ALIGNMENTS

RESULT 1
Q91WR1
ID Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 53.0 kDa protein.
GN AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -.
DR MGD; MGI:2144917; AI893585.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 78.4%; Score 76; DB 11; Length 488;
Best Local Similarity 81.2%; Pred. No. 0.00041;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16
||:|||||
Db 69 DINPYNGGTSYNQKFK 84

RESULT 2
Q8VCV5
ID Q8VCV5 PRELIMINARY; PRT; 481 AA.
AC Q8VCV5;

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RT "Octopine-type Ti plasmid sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242881; AAB88471.1; -.
DR InterPro: IPR003692; Hydantoinase_B.
DR Pfam: PF02538; Hydantoinase_B; 1.
KW Plasmid.
SQ SEQUENCE 550 AA; 59345 MW; 73E3208B03886CF8 CRC64;

Query Match 70.7%; Score 41; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSFTDYF 8
|||||
Db 231 YSFTDYF 237

RESULT 13
Q96LU7
ID Q96LU7 PRELIMINARY; PRT; 275 AA.
AC Q96LU7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ25056 fis, clone CBL04463.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK057785; BAB71571.1; -.
SQ SEQUENCE 275 AA; 31228 MW; 74EF60D529BA27BB CRC64;

Query Match 69.0%; Score 40; DB 4; Length 275;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
| |||||
Db 260 GIFFTDYFFY 269

RESULT 14
O63624
ID O63624 PRELIMINARY; PRT; 310 AA.
AC O63624;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
GN ND1.
OS Dalbulus cimmyti.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracoidea; Cicadellidae; Deltocephalinae; Dalbulus.
OX NCBI_TaxID=74060;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
Phylogeny based on Mitochondrial DNA sequences."
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

CC -I- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
DR EMBL: AF051290; AAC05754.1; -.
DR InterPro: IPR001694; Resp_NADH_dh1.
DR Pfam: PF00146; NADHdh; 1.
DR PROSITE: PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE: PS00668; COMPLEX1_ND1_2; 1.
KW Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
SQ SEQUENCE 310 AA; 36056 MW; FFF22BB436C442F5 CRC64;

Query Match 69.0%; Score 40; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
||| ||| |
Db 160 YSFMDYFSY 168

RESULT 15
O63626
ID O63626 PRELIMINARY; PRT; 310 AA.
AC O63626;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
GN ND1.
OS Dalbulus elimatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracoidea; Cicadellidae; Deltocephalinae; Dalbulus.
OX NCBI_TaxID=74070;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
Phylogeny based on Mitochondrial DNA sequences."
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -I- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
DR EMBL: AF051292; AAC05756.1; -.
DR InterPro: IPR001694; Resp_NADH_dh1.
DR Pfam: PF00146; NADHdh; 1.
DR PROSITE: PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE: PS00668; COMPLEX1_ND1_2; 1.
KW Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
SQ SEQUENCE 310 AA; 36327 MW; 4C8E3BDF2C0A38AE CRC64;

Query Match 69.0%; Score 40; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
||| ||| |
Db 160 YSFLDYFSY 168

Search completed: March 10, 2003, 17:00:12
Job time : 24.069 secs

KW Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
SQ SEQUENCE 310 AA; 36155 MW; 14947B09CAA1B4B1 CRC64;

Query Match 70.7%; Score 41; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
||| ||| |
Db 160 YSFMDYFYY 168

RESULT 9
O63635
ID O63635 PRELIMINARY; PRT; 310 AA.
AC O63635;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
OS Baldulus tripsaci.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracoidae; Cicadellidae; Deltocephalinae; Baldulus.
OX NCBI_TaxID=74058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPECIMEN ONE;
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
Phylogeny based on Mitochondrial DNA sequences.";
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
DR EMBL; AF051301; AAC05765.1; -.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Mitochondrion.
SQ SEQUENCE 310 AA; 36364 MW; C464DF7484DB66E7 CRC64;

Query Match 70.7%; Score 41; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
||| ||| |
Db 160 YSFMDYFYY 168

RESULT 10
O63636
ID O63636 PRELIMINARY; PRT; 310 AA.
AC O63636;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
OS Baldulus tripsaci.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracoidae; Cicadellidae; Deltocephalinae; Baldulus.
OX NCBI_TaxID=74058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPECIMEN TWO;
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
Phylogeny based on Mitochondrial DNA sequences.";
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
DR EMBL; AF051302; AAC05766.1; -.

DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Mitochondrion.
SQ SEQUENCE 310 AA; 36519 MW; CE7B3A4CA4B5FE70 CRC64;

Query Match 70.7%; Score 41; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
||| ||| |
Db 160 YSFMDYFYY 168

RESULT 11
Q91WT1
ID Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 70.7%; Score 41; DB 11; Length 481;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
||: || | : |
Db 45 GYTFTSYIYH 54

RESULT 12
O50266
ID O50266 PRELIMINARY; PRT; 550 AA.
AC O50266;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Agag.
GN AGAG.
OS Agrobacterium tumefaciens.
OG Plasmid Ti.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99141607; PubMed=9987134;
RA Lyi S.M., Jafri S., Winans S.C.;
RT "Mannopinic acid and agropinic acid catabolism region of the octopine-
type Ti plasmid pTi15955.";
RL Mol. Microbiol. 31:339-347(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
RA Farrand S.K.;

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OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match      72.4%; Score 42; DB 11; Length 117;
Best Local Similarity 66.7%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
Db 26 GYTFTDYIM 34

RESULT 6
Q9SNT3
ID Q9SNT3 PRELIMINARY; PRT; 586 AA.
AC Q9SNT3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Similar to Arabidopsis thaliana DNA chromosome 4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone:P0538C01.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP000391; BAA83364.1; -.
DR InterPro; IPR004331; SPX.
DR Pfam; PF03105; SPX; 1.
SQ SEQUENCE 586 AA; 65924 MW; DA2D51DCBFD8C929 CRC64;

Query Match      72.4%; Score 42; DB 10; Length 586;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
Db 136 GYRFTDYIV 144

RESULT 7
Q8X4Z9
ID Q8X4Z9 PRELIMINARY; PRT; 253 AA.
AC Q8X4Z9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ARAC-type regulatory protein.
GN z2209 OR ECS2104.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
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OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005355; AAC56269.1; -.
DR EMBL; AP002557; BAB35527.1; -.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF00165; HTH_ARAC; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Complete proteome.
SQ SEQUENCE 253 AA; 28885 MW; E77C92CDAC94B9CC CRC64;

Query Match      70.7%; Score 41; DB 16; Length 253;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 208 GYASTSYFIY 217

RESULT 8
O63625
ID O63625 PRELIMINARY; PRT; 310 AA.
AC O63625;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
GN NDI.
OS Dalbulus ebberti.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracoidea; Cicadellidae; Deltocephalinae; Dalbulus.
OX NCBI_TaxID=74061;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
RT Phylogeny based on Mitochondrial DNA sequences.";
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
DR EMBL; AF051291; AAC05755.1; -.
DR InterPro; IPR001694; Resp_NADH_dh1.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_NDI_1; 1.
DR PROSITE; PS00668; COMPLEX1_NDI_2; 1.
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